STIC-Biotech/ChemLib

From:	
Sent:	
OCIIL.	
T	

Jiang, Dong

Thursday, August 22, 2002 2:10 PM

To: Subj ct: STIC-Biotech/ChemLib

09/854,208

Priority: 5/4/99 Chen (Genetech)

Please search SEQ ID NO:3

-issued

-commercial

no art.

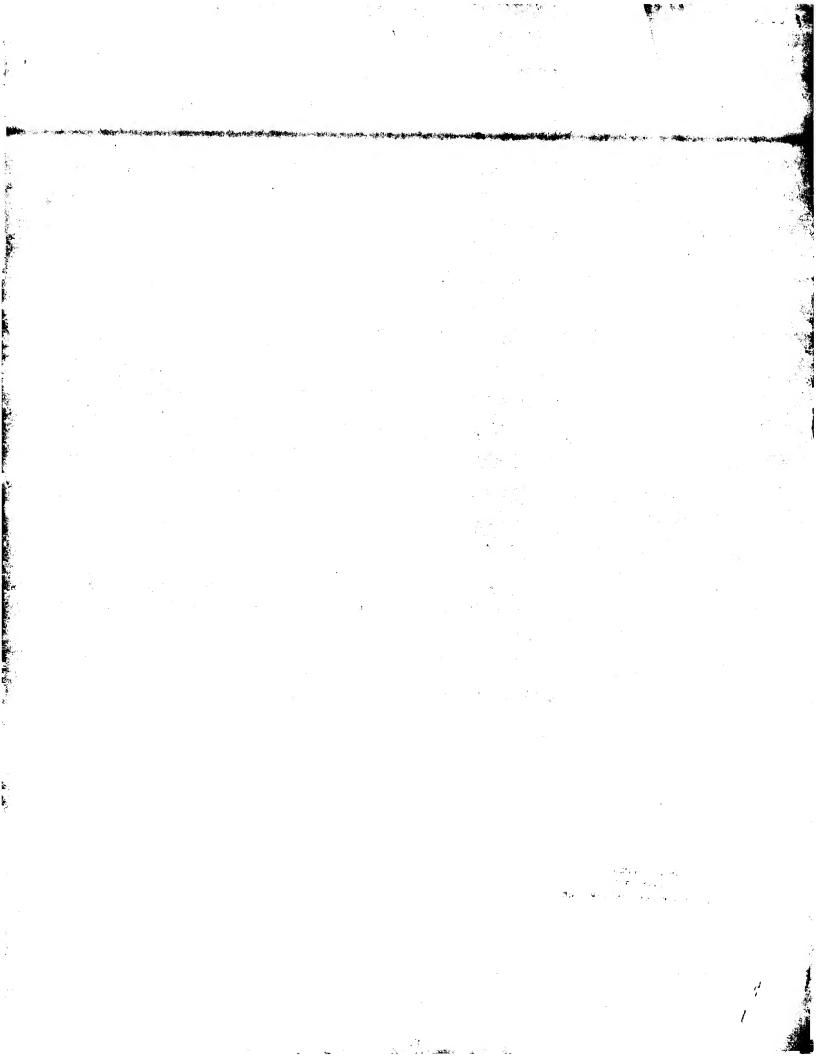
Please send results on paper to Dong Jiang in 10D-08 (mail stop CM1-10D19). Thank you very much.

Dong Jiang (78243)
703-305-1345
U.S. Patent and Trademark Office
Art Unit 1646
dong.jiang@uspto.gov
CM1-10D08
Mail stop: CM1-10D19

Searcher: Point of Contact
Phone: P. Sheppard
Location in P. Sheppard
Location

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):



```
August 23, 2002, 16:00:49 ; Search time 29.85 Seconds (without alignments) 733.050 Million cell updates/sec
                                                                                                                                                                                                                                                             1 MTLLPGLLFLTWLHTCLAHH......FHTEFIHVPVGCTCVLPRSV 197
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                         747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                    US-09-854-208-3
1073
                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                             Run on:
```

1: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*
7: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
9: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
10: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
11: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
14: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
15: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
16: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
17: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
18: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
19: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
19: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
20: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

			Description	A novel polypeptid	A human interleuki	A human interleuki	Human interleukin-	Human Interleukin	Amino acid sequenc	Human interleukin	Human PRO polypept	Human Interleukin	Human Interleukin	Human Interleukin
SUMMARIES			qi	AAB18911	AAB07602	AAB07684	AAY92238	AAY4460	AAY53892	AAG66121	AAU29247	AAU04951	AAY44485	AAY44462
			DB	21	21	21	21	21	21	22	22	22	21	21
		Query	Length	197	197	197	197	197	197	197	197	197	206	425
	dР	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
			Score	1073	1073	1073	1073	1073	1073	1073	1073	1073	1073	1073
		Result	No.	1	7	е	4	ა	9	7	80	σ	10	11

WO200056889-A2.

ΡN

	Human interleukin A human interleukin	ALIGNMENTS ated PRO1122. brane protein; PRO1484; PRO4334; PRO1122; PRO4405; PRO4405; PRO4405; PRO4405; PRO4409; PRO5409; PRO540
AAE08676 AAE08681 AAE08681 AAE08681 AAE08687 AAE08687 AAE08686 AAE08690 AAE08690 AAE08690 AAE08690	AAEC08099 AAEC08701 AAEC08701 AAEC08696 AAEC08696 AAEC08696 AAEC08702	ALIGNMENTS 1; 2001 (first entry) polypeptide designated PR01122. protein; transmembrane protein; protein; transmembrane protein; pro422; PR04430; PR04409; tumouemia; kidney disorder; Bergers disorder; Bergers disorder, Bergers disorder, Bergers disorder, Bergers disorder, Bergers disorder; Bergers disorder; Bergers disorder; Bergers disorder; Bergers disorder; Bergers disorder. Location/Qualifiers 118 /note= "signal peptide" 3238 /note= "leucine zipper pa 3238 /note= "N-myristoylation forte 112121 /note= "N-myristoylation forte 112121 /note= "Lyrosine kinase passite 133139
		in; y) gnat gnat 7; P
222 222 222 222 222 222 222 222 222 22	227 227 227 227 227 227 227 87 87 123 123 202 202	d; Protein; 197 .rst entry) .ide designated P .ide designated P .ipen1887; PR044 .ipen2887; PR044 .ipen3847; PR044 .ipen3847; PR044 .ipen48367; PR044 .ipen4887; PR044 .ipen4887; PR044 .ipen2887; PR044 .ipen28887; PR044 .ipen2888888888888888888888888888888888888
40.00.00.00.00.00.00.00.00.00.00.00.00.0		tandard; lypeptid lypeptid rotein; RO4380; RO4422; RO
00000000000000000000000000000000000000	y o o o o o o o o o o o o o o o o o o o	standard; 001 (firs polypeptid protein; PRO4380; PRO4380; PRO4380; PRO4422; mid; kidne mid; kidne n-Henoch p isease. Lo iens. Lo iens. -site 32 -site 55 -site 55 -site 55
1063 1060 1060 1060 1059 1058 1058 1058 1058 1058 1058 1058	10054 10054 10053 10053 10053 10053 10053 10053 10054 10054 10054 10054 10054 10054 10054 10054 10054 10054 10054 10054 10054	1 1891. 1891. 1891. 1893. 1835. 1835. 1835. 1836
112 122 133 144 154 155 156 157 157 157 157 157 157 157 157 157 157	00000000000000000000000000000000000000	ARESULT AAB18911 AAB18911 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
		A A B B B B B B B B B B B B B B B B B B

~

```
a
                                                                                                                                                                                                                                                                                 q
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes polypeptides designated PRO1484, PRO4334, PRO4122, PRO1889, PRO1890, PRO1887, PRO4486, PRO4334, PRO4122, PRO4189, PRO1890, PRO1896, PRO4818, PRO4405, PRO4405, PRO4036, PRO4036, PRO4036, PRO4036, PRO4036, PRO4036, PRO4036, PRO4036, PRO40405, PRO4040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a secreted or transmembrane polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel secreted and transmembrane polypeptides useful for diagnosing tunnour in a mammal, for identifying agonists and antagonists of the polypeptide and for therapeutic use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1073; DB 21; Length 197; 100.0%; Pred. No. 4.6e-109; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Godowski PJ,
Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goddard A,
Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Fig 6; 222pp; English.
                                                                                                            99US-0125778.
99US-0125826.
99US-0127035.
                                                                                                                                                                                                                                99US-0131270
99US-0131272
                                       2000WO-US05601
                                                                                                                                                                                                                                                                               99US-0131291
99US-0132371
                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0146970
                                                                                                                                                                                   99US-0127706
                                                                                                                                                                                                            99US-0130359
                                                                                                                                                                                                                                                                                                                             99US-0132379
99US-0132383
                                                                                                                                                                                                                                                                                                                                                                               99US-0135750
                                                                                                                                                                                                                                                                                                                                                                                                     99US-0138166
                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0144791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0170262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eaton DL, G
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-628263/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAA96338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Desnoyers L,
Stewart TA,
                                       01-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-1999;
09-DEC-1999;
                                                                                                                                     24-MAR-1999
31-MAR-1999
                                                                                                                                                                                   05-APR-1999
                                                                                                                                                                                                            21-APR-1999
                                                                                                                                                                                                                                27-APR-1999,
27-APR-1999,
                                                                                                                                                                                                                                                                                                                             04-MAY-1999
04-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                            25-MAY-1999
08-JUN-1999
                                                                                                                                                                                                                                                                                 27-APR-1999
                                                                                                                                                                                                                                                                                                       04-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
```

```
The present sequence represents an interleukin-171 (IL-171) polypeptide. The polypeptide is.an IL-17-11ke (CTLA-8 related) protein. It is a member of a new group of interleukins, IL-170 polypeptides. The member comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170 protein can be used to treat abnormal proliferation e.g. cancer or degenerative conditions. Antibodies can be used in diagnostic methods to detect over production of IL-170 protein in cells or body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFFT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide encoding a mammalian Interleukin-17 like
                                                                                                                                                                                                                                                                                                                                                    Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;
IL-177; IL-171; cell proliferation; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1073; DB 21; Length 197; 100.0%; Pred. No. 4.6e-109; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to identify genes for homologous proteins
                                                                                                                                                                                                                                                                                                          A human interleukin (IL) 171 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..17
/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 20-21; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kastelein RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                  AA.
                                                                                                                                                                AAB07602 standard; Protein; 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JAN-2000; 2000WO-US00006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0228822
                      181 efihvpvgctcvlprsv 197
181 EFIHVPVGCTCVLPRSV 197
                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0
Best Local Similarity 100.0
Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18..197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bazan JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-466130/40.
N-PSDB; AAA58991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200042188-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein used
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-1999;
                                                                                                                                                                                                                                                              07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gorman DM,
                                                                                                                                                                                                               AAB07602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                          AAB07602
```

ó

g ò q ò

ò

셤

g

ò

```
AAY92238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY92238
ID AAY9
                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                              g
                                                                                ΟŻ
                                                                                                                                  g
                                                                                                                                                                                 Qγ
                                                                                                                                                                                                                                                                                             ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL-171 protein, antibodies against IL-171, montages protein, antibodies against IL-171, and compounds which have binding affinity to IL-171 are useful in treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions, or degenerative conditions. The IL-171 protein can be used in kits and assay methods for identifying compounds that selectively bind to IL-171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA sequence encoding a mammalian homolog of CTLA-8, designated interleukin-171 (IL-171), useful for recombinant production of IL-171 which can be used for treating conditions associated with abnormal physiology or development.
121 pqklafaeclcrgcidartgretaalnsvrllqsllvlrrrpcsrdgsglptpgafafht 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;
IL-174; IL-176; IL-177; cell proliferation; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents an interleukin (IL)-171 polypeptide. It is a mammalian homologue of the cytokine designated CTLA-8 (also referred to as IL-17). The specification also describes homologues IL-171, IL-175, IL-173, IL-174, IL-176, and IL-177. The DNA sequence encoding IL-171 is useful for identifying genes, mRNA and CDNA molecules which code for related or homologous proteins. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "putative glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 10-11; 111pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kastelein RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                A human interleukin-171 polypeptide.
                                                                                                                                                                                                                                     AAB07684 standard; Protein; 197 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JAN-2000; 2000WO-US00005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0229402
                                                    EFIHVPVGCTCVLPRSV 197
                                                                          181 efihvpvgctcvlprsv 197
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18..197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
55..57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gorman DM, Bazan JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-476060/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA59149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200042187-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                              07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUL-2000
                                                                                                                                                                                                                                                                                       AAB07684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                    181
                                                                                                                                                                                                               AAB07684
```

```
neutrophils, granulocýtes, or platelets, this may be useful during chemcherapy. IL-17 homologues have at least one activity selected from induction of cytotoxic T cells, induction of lymphokine-activated killer cell proliferation or a B or T cell stimulation. The IL-17 homologue may also be used to treat viral or bacterial infections, immune related diseases, anemia, leukemia, thrombocytopenia, uremia, Von Willebrand disease, postoperative cardiovascular dysfunction, treatment of AIDS (acquired immune deficiency syndrome)-related bone marrow failure, and inflammatory diseases of the gastrointestinal system, joints, and lungs.
                                                         120
                                                                                                 121 PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT 180
               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding an interleukin-17 (IL-17) homolog polypeptide which enhances hematopoiesis, useful for treating e.g. anemia, thrombocytopenia, viral and bacterial infections
61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin 17 (IL-17) stimulates hematopoiesis and production of
                                                                                                                                                                                                                                                                                                                                                                          Interleukin 17; IL-17; haematopoiesis; chemotherapy; cytostatic; antianemic; cardiant; hemostatic; anti-inflammatory; anti-HIV.
                                                                                                                                                                                                                                                                                                                                               Human interleukin-17 (IL-17) homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= signal_peptide
19.197
/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 16; Page 92-93; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                           AAY92238 standard; Protein; 197 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wei J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0110405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US22678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0102883
                                                                                                                                                                        181 efihvpvgctcvlprsv 197
                                                                                                                                                         181 EFIHVPVGCTCVLPRSV 197
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Su EW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   & CO BLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-303778/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA09153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glasebrook AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200020593-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIL ) LILLY
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-1998;
                                                                                                                                                                                                                                                                                                                    10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1998;
11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-APR-2000
```

Query Match 100.0%; Score 1073; DB 21; Best Local Similarity 100.0%; Pred. No. 4.6e-109; Matches 197; Conservative 0; Mismatches 0;

.197 AA;

Sequence

0;

0;

DB 21; Length 197; Indels

```
(first entry)
                                                                                                                                                                                                                                                                                 181 EFIHVPVGCTCVLPRSV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63..68
/note= "c,
104..109
/note= "c,
113..121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
WPI; 2000-116314/10.
N-PSDB; AAZ29728.
                                                                                                                                         197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                13-MAR-2000
                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                  AAY53892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                           AAY53892
qq
                                                                                                                                                                                                                       Qγ
                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                    ...ceileuxin; IL-17C; PRO1122 polypeptide; clone DNA62377-1381-1; UNQ561; cytokine IL-17; cytotoxic T-lymphocyte-associated antigen 8; CTLA-8; hybridisation probe; antagonist; degenerative cartilaginous disorder; agonist; diagnose; therapy.
                                                                               61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 120
                                                                                                    121 PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT 180
                            Gaps
                                                         9
                                                  1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGOAPPHLLARGAKWGO
                                                                                                                                                                                                                                                                                                    1..18
7.label- Signal_peptide
19..197
7.label- Mature_IL-17C_polypeptide
/note- "Used to treat degenerative cartilaginous
                            ó
             Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wood WI;
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H
             DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ľ
                     Pred. No. 4.6e-109
                                                                                                                                                                                                                                                                                                                                                        'note= "Conserved Trp residue"
                                                                                                                                                                                                                                                                                                                                                                                                                 residue'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL,
                                                                                                                                                                                                                            Human Interleukin 17C, PRO1122 polypeptide.
             Score 1073;
                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gurney
                                                                                                                                                                                                                                                                                                                                                                       Cys
                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Conserved Cys
191
                                                                                                                                                                                                                                                                                                                                                                                     Cys
                                                                                                                                                                                                                                                                                                                                                                                                  'note- "Conserved Cys
                                                                                                                                                                                                                                                                                                                                                                                                                               "Conserved Cys
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                  AAY44460 standard; Protein; 197 AA.
                                                                                                                                                                                                                                                                                                                                                                      'note= "Conserved
                                                                                                                                                                                                                                                                                                                                                                                    /note= "Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard A,
                           ;
             100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US10733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0085579.
                                                                                                                                EFIHVPVGCTCVLPRSV 197
                                                                                                                                        efihvpvgctcvlprsv 197
                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                         disorder"
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Filvaroff E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                               Misc-difference 129
                    al Similarity
197; Conserv
                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9960127-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L5-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-1998;
                                                                                                                                                                                                               27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-NOV-1999
                                                                                                                                                                                                 AAY44460;
             Query Match
                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen J,
                                                                                                                                              181
                            Matches
                                                                                                                                181
                                                                                                                                                                           AAY44460
                                                                                                                                                                                                 g
                                                        g
                                                                       ò
                                                                                    q
                                                                                                  õ
                                                                                                                                ò
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; interleukin-22; IL-22; IL-21; immune system disorder; immune cell chemotaxis; haematopoietic cell disorder; haemstatic activity; thrombolytic activity; autoimmune disorder; asthma; respiratory problem; organ rejection; graft-versus-host disease; GVHD; inflammation; hyperproliferative disorder; tissue regeneration; embryonic stem cell differentiation; embryonic stem cell proliferation; haematopoietic lineage; allergic asthma.
                                                                                                                                                                                                The present sequence is the human PRO1122 polypeptide, also referred to as UNO561, and as interleukin-17C (IL-17C), encoded by clone DNA62377-1381-1. This sequence has identity with the cytokine IL-17 and cytotoxic T-1ymphocyte-associated antigen 8 (CTLA-8) and has leucine zipper pattern. PRO1122 is expressed in pancreas, small intestine, stomach and testis also. It shares about 26-28% amino acid identity with IL-17 and IL-17E. The entire coding region of IL-17C can be used as hybridisation probe. The PRO1122 polypeptide, agonist or antagonist, is used to diagnose and treat a degenerative cartilaginous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpvalvssleaashrgrherpsattqcpvlrpeevleadthqrsispwryrvdtdedry 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1073; DB 21; Length 197; Best Local Similarity 100.0%; Pred. No. 4.6e-109; Matches 197; Conservative 0; Mismatches 0; Indels 0;
New polypeptides designated \mathsf{PRO1031} and \mathsf{PRO1122} used to treat degenerative cartilaginous disorder -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "conserved domain VII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of human interleukin-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "conserved domain VI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "conserved domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.18
/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                        Claim 23; Fig 3; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY53892 standard; Protein; 197
```

S

(first entry)

```
Human interleukin (IL)-21 amino acid sequence.
                              AAG66121 standard; Protein; 197 AA.
                                                                      13-MAR-2002
                                                  AAG66121;
                                                                                                                                                                             Peptide
                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                  Domain
          RESULT
AAG66121
                                                                                                                                                                    Key
                                         The present sequence represents a human interleukin-21 (IL-21) protein. The specification also describes IL-22 polynucleotides and polypeptides. The IL-21 polynucleotide was isolated from a cDNA library of apoptotic T-cells. IL-21 and IL-22 may be useful in treating of deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells, treating or detecting deficiencies or disorders of haematopoletic cells, to modulate haemostatic or treating asthma (particularly allergic asthma) or other respiratory problems, to treat and/or prevent organ rejection or graft-versus-host disease (GWHD), to modulate inflammation, to treat or detect infectious agents, to disease (GWHD), to modulate inflammation, to detect infectious agents, to differentiate, proliferate and attract cells, leading to the differentiation or proliferation of embryonic stem cells and the content of the differentiation or proliferation of embryonic stem cells and the content and and the mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                e.g. immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1073; DB 21; Length 197; Pred. No. 4.6e-109;
                                                                                                                                                                                                                                                             Novel polynucleotides used to develop products for treating disorders, blood disorders, autoimmune disorders, allergies, inflammation, hyperproliferative disorders or infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                  /note= "conserved domain II"
156..162
/note= "conserved domain III"
1185..192
/note= "conserved domain IV"
"conserved domain I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                      Claim 26; Fig 6A-B; 170pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
100.0%;
                                                                                                                                           98US-0087340.
98US-0099805.
99US-0131965.
                                                                                                                                                                                      HUMA-) HUMAN GENOME SCI INC
                                                                                                                         99WO-US11644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             efihvpvgctcvlprsv 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFIHVPVGCTCVLPRSV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0
Best Local Similarity 100.0
Matches 197; Conservative
        .134
 /note=
                                                                                                                                                                                                                               WPI; 2000-072622/06.
                                                                                                                                                                                                           Ebner R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 AA;
                                                                                                                                                                                                                                          N-PSDB; AAZ36836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           characteristics.
                                                                                 WO9961617-A1.
                                                                                                                        27-MAY-1999;
                                                                                                                                             29-MAY-1998;
                                                                                                                                                       10-SEP-1998;
                                                                                                                                                                 30-APR-1999;
                                                                                                    02-DEC-1999
                                                                                                                                                                                                           Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
          Domain
                              Domain
                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
The invention relates to novel human proteins designated interleukin (IL)-21 and IL-22. The IL-21 and IL-22 polynucleotides can be used in linkage analysis as a marker for those specific chromosome, in chromosome mapping, to control gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, in identifying individuals from minute biological samples, as an alternative to restriction fragment length polymorphism (RFLP) analysis, as polymorphic markers for forensic purposes, as molecular weight markers, or as diagnostic probes. IL-21 and IL-22 polypeptides can be used to treat, prevent or diagnose diseases of the immune system by activating or inhibiting the proliferation,
Interleukin; IL-21; IL-22; immunosuppressive; cytostatic; thrombolytic; antlinflammatory; antibacterial; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New interleukin-21 and interleukin-22 polynucleotides and polypeptides, useful for treating, preventing or diagnosing e.g. disorders of hematopoietic cells, autoimmune disorders, or hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                               104...109
/note= "conserved domain VII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "conserved domain III"
                                                                                                                                                                                                                                                                                                                                                              /note= "conserved domain VI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "conserved domain II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "conserved domain IV"
                                                                                                                                                                                                                                                                             34..40
/note= "conserved domain V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "conserved domain I"
                                                                                                                                                                                                                                           /note= "mature protein"
                                                                                                                                                                                       /note= "signal peptide"
                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 26; Fig 6A-B; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-087340P.
99US-131965P.
99US-169837P.
99US-0320713.
99WO-US11644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-DEC-2000; 2000US-0731816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "c
185..192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129..134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156..162
                                                                                                                                                                                                                       19..197
                                                                                                                                                                                                                                                                                                                                    63..68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-638470/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ebner R, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S.
M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAI67878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2001023070-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EBNE/) EBNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RUBE/) RUBEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAY-1998;
30-APR-1999;
09-DEC-1999;
27-MAY-1999;
                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases
```

o

```
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pp
                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; plg; goat; rabblt; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
differentiation or mobilization of immune cells, disorders of hematopoietic cells (e.g. ataxia, human immunodeficiency virus (HIV) infection, anemia, thrombocytopenia), autoimmune disorders (e.g. Grave's disease, systemic lupus erythematosus, ophthalmia), graft versus host disease, inflammation, hyperproliferative disorders, or infectious can be used to treat, inhibit or prevent diseases or conditions associated with aberrant expression and/or activity of IL-21 or IL-22. The present sequence represents the amino acid sequence of human IL-21.
                                                                                                                                                                                                       61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 120
                                                                                                                                                                                                                                              121 PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT 180
                                                                                                                                                                                                                                                                180
                                                                                                                                                Gaps
                                                                                                                                                                                     9
                                                                                                                                                                             1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ
                                                                                                                                                                                                                                                       0;
                                                                                                                               Length 197;
                                                                                                                                                0; Indels
                                                                                                                             100.0%; Score 1073; DB 22;
100.0%; Pred. No. 4.6e-109;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO polypeptide sequence #224.
                                                                                                                                                                                                                                                                                                                                                     AAU29247 standard; Protein; 197 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-US06884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-192655P.
2000US-193032P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-187202P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-189320P.
2000US-189328P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-190828P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-191007P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-19104BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-191314P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-193053P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2001; 2001WO-US06520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-194449P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US05601
2000WO-US05841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-US08439
                                                                                                                                                                                                                                                                                              181 EFIHVPVGCTCVLPRSV 197
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                               Matches 197; Conservative
                                                                                                                                       Similarity
                                                                                                197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200168848-A2
                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-2000;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                        AAU29247;
                                                                                                 Sequence
                                                                                                                              Query Match
                                                                                                                                      Best Local
                                                                                                                                                                                                                                                                                                                                            AAU29247
                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                          q
   à
                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                      g
```

```
Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the and a control sample of normal cells, whereby a higher level of and a control sample of normal cells, whereby a higher level of mammal. Mammals include dogs, cats, catle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gurney AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQKLAFAECL.CRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     susceptibility to tumour development, particularly adrenal, lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goddard A, Gouc-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1073; DB 22; 100.0%; Pred. No. 4.6e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Fig 448; 774pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desnoyers L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                o, Chen J, Desnoyers L
Smith V, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·
0
20000S-196000P.
20000S-196187P.
20000S-196690P.
20000S-196820P.
2000US-198121P.
                                                                                                                                                                                                                    2000US-201516P.
2000WO-US13705.
2000WO-US14042.
                                                                                                                        2000US-198585P
                                                                                                                                                   2000US-199397P
                                                                                                                                                                       2000US-199550P.
2000US-199654P.
                                                                                                                                                                                                                                                                                                                                                                 2000WO-US20710
2000US-0644848
                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-US23328
2000WO-US30952
                                                                                                                                                                                                                                                                                             2000WO-US14941
                                                                                                                                                                                                                                                                                                                      2000WO-US15264
                                                                                                                                                                                                                                                                                                                                             2000US-209832P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-US34956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-602746/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 197; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS46148
                                                                                                                                                                                                                                                                                                                    02-JUN-2000;
05-JUN-2000;
28-JUL-2000;
                                                  11-APR-2000;
                                                                           11-APR-2000;
                                                                                                 18-APR-2000;
                                                                                                                        18-APR-2000;
                                                                                                                                                   25-APR-2000;
                                                                                                                                                                       25-APR-2000;
                                                                                                                                                                                                                       03-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2000;
20-DEC-2000;
                                                                                                                                                                                              25-APR-2000;
                                                                                                                                                                                                                                                17-MAY-2000;
                                                                                                                                                                                                                                                                         22-MAY-2000;
                                                                                                                                                                                                                                                                                             10-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                           24 - AUG - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
```

ö

```
The sequence is PRO1122 which is the human Interleukin 17C ligand,
IL-17C, encoded by DNA 62377-1381-1. A composition
Containing ant/agonists to the PRO polypeptides or individual components
are useful for treating a mammal with an immune related disease, e.g.
ivenile chronic arthritis, a spondyloarthropethy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogran's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
C thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease, an autoimmune or immune-mediated skin disease, contact dermatitis, an allergic disease e.g. food
C thronic inflammatory demyelinating polyneuropathy. Treating a profile degenerative cartilaginous disorder comprises administering a PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous
C examples of the diseases and disorders are given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoprecipitation; IL-17 receptor extracellular domain; IL-17R ECD; cytokine IL-17, hybridisation probe; antagonist; Gly(His)8 tag; agonist; degenerative cartilaginous disorder; diagnose; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 120
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interleukin; IL-17C.his; PRO1122 polypeptide; clone DNA62377-1381-1;
Novel PRO polypeptides homologous to interleukin-17, useful for the diagnosis and treatment of immune related disease e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                 1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..18
/label= Signal_peptide
19..197
/label= Mature_IL-17C_polypeptide
/note= "Used to treat degenerative cartilaginous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Interleukin 17C with C-terminal Gly(His)8 tag, IL-17C.his.
                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                Length 197;
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1073; DB 22; 100.0%; Pred. No. 4.6e-109; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Conserved Trp residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY44485 standard; Protein; 206 AA.
                                                   Claim 10; Fig 4; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              efihypygctcylprsv 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 EFIHVPVGCTCVLPRSV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 100.
Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder"
                          arthritis and diabetes
                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                        197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY44485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
                                                                                                                                                                                                                        PRO1122; DNA 62377-1381-1; systemic lupus erythematosus;
Theumatoid arthritis; osteoarthritis; diabetes mellitus;
allergic disease; asthma; demyelinating disease;
degenerative cartilaginous disorder; transplantation associated disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grimaldi CJ;
Vandlen RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                            Human; Interleukin-17C ligand; IL-17C; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard A, Godowski PJ,
Tumas D, Van Lookeren M,
od WI, Yansura DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               99...125
/note= "Region homologous to IL-17"
                                                                                                                                                                                                                                                                                                                                                                      "Leucine zipper pattern"
                                                                                                                                                                                                                                                                                                                                                                                                                            "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                               1..18
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                 /label= Mature_IL_17C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Filvaroff E, Fong S, Godda
L, Li H, Hillan KJ, Tumas
CK, Williams PM, Wood WI,
                                                                                                                                                                                  Human Interleukin 17C ligand, IL-17C.
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                      ¥.
                                                                                                     AAU04951 standard; Protein; 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WO-US34956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0172096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US31274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000WO-US07532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000WO-US15264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  000US-0644848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000WO-US23328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0242837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         000WO-US30873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0253646
2000WO-US32678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0175481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US04341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-US05841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0191007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0213087
                       Watanabe CK, Williams PM,
            EFIHVPVGCTCVLPRSV 197
                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .139
                                                                                                                                                                                                                                                                                                                                                                                    197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
133..13
                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-451708/48.
N-PSDB; AAS09510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200146420-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2000;
21-MAR-2000;
02-JUN-2000;
                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 - AUG - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 -OCT - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-NOV-2000;
                                                                                                                                                        24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AĽ,
                                                                                                                               AAU04951;
                                                                                                                                                                                                                                                                                                                    Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen J,
                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gurney
                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                            6
            181
                                                                                       AAU04951
                                    g
            ò
```

; 0

ø

```
WO9960127-A2
                                                    Homo sapiens
                                                                                                                                                                                                                                                                                             14-MAY-1999;
                                                                                                                                                                                                                                                                                                              15-MAY-1998;
                                                                                                                                                                                                                                                                                                                       23-DEC-1998;
                                                                                                                                                                                                                                                                             25-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                           Peptide
                                                                                              Protein
                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                   The present sequence is the human PRO1122 polypeptide, with a C-terminal G1/His) B tag, IL-17C.his, derived from the clone DNA62377-1381-1.
This sequence is used in a competitive binding experiment for the immunoprecipitation of IL-17 receptor extracellular domain (IL-17R ECD). The entire coding region of IL-17C can be used as hybridisation probe. The PRO1122 polypeptide, agonist or antagonist, is used to diagnose and treat a degenerative cartilaginous disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 120
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGOAPPHLLARGAKWGO
                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                              Length 206;
                                                                                                                                                                                                                                          polypeptides designated PRO1031 and PRO1122 used to treat
                                                                                                                                                                                                          Wood
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                                                                                                             tch 100.0%; Score 1073; DB 21; al Similarity 100.0%; Pred. No. 4.9e-109; 197; Conservative 0; Mismatches 0;
                                                                                                                                                                                                         ij
                                                                                           /note= "C-terminal Gly(His)8 tag"
                                                           residue"
        "Conserved Cys residue"
                                                                                                                                                                                                         Gurney AL,
                                                                                                                                                                                                                                                                   Example 11; Page 138-139; 141pp; English.
                                  /note= "Conserved Cys
189
                                                         /note= "Conserved Cys
                                                                          'note= "Conserved Cys
                         'note= "Conserved Cys
                                                                                                                                                                                                                                                    degenerative cartilaginous disorder
                                                                                                                                                                                                         Goddard A,
                                                                                                                                                              98US-0085579.
                                                                                                                                              99WO-US10733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY4462 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 EFIHVPVGCTCVLPRSV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                    Misc-difference 198..206
         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Filvaroff E,
                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                         WPI; 2000-116314/10
Misc-difference 129
                                 Misc-difference 163
                                                                  Misc-difference 191
                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                       206 AA;
                                                  Misc-difference
                                                                                                             WO9960127-A2
                                                                                                                                              14-MAY-1999;
                                                                                                                                                              15-MAY-1998;
23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY44462;
                                                                                                                                                                                                         Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY4462
ID AAY4
XX AC AAY4
XX DT 27-b
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the human IL-17C.fc fusion protein, derived from PRO1122 polypeptide and the Fc region of human 19G1. The cytokine IL-17C can be used to induce the release of TNF-alpha from human leukemic monocytic, THP-1 cells. The fusion protein, IL-17C.fc is used to identify the binding of IL-17C to THP-1 cells, using fluoresence-activated cell sorter analysis (FACS).
                                              Interleukin; IL-17C.fc; fusion protein; PRO1122 polypeptide; cytokine; human IgG1; fluoresence-activated cell sorter analysis; FACS; Tumour Necrosis Factor-alpha; TNF-alpha; leukemic monocyte; THP-1 cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197..425
/note= "Sequence derived from Fc region of human IgG1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ
                                                                                                                                                                                                                                                                                          /label= Mature_IL-17C_polypeptide
/note= "Used to treat degenerative cartilaginous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptides designated PRO1031 and PRO1122 used to treat
Human Interleukin 17C-IgG1 Fc fusion protein, hIL-17C.fc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ľį
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1073; Db 2...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Conserved Cys residue"
197..425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Conserved Cys residue"
                                                                                                                                                                                                                                                                                                                                                                                            /note= "Conserved Trp residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Conserved Cys residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Conserved Cys residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 12; Page 129-130; 141pp; English
                                                                                                                                                                                                                       1..18
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Conserved Cys
Misc-difference 191
                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 degenerative cartilaginous disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US10733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0085579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0113621
                                                                                                                                                                                                                                                                                                                                                disorder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                        19..197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen J, Filvaroff E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-116314/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 197; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425 AA;
                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
```

σ

```
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 - NOV - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .6-AUG-2001
                                                                                                                                        Matches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                AAE08680;
                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jing S,
                                                                                                                                                                                                                63
                                                                                                                                                                                                                                         93
                                                                                                                                                                                                                                                                                                                                                                                            AAE08680
                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                        q
 SSSSSXS
                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                 δy
                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                     and nucleic acids encoding them. IL-17 like protein is useful for identifying binding partners, agonists and antagonists which can be used for treating one or more diseases or discorders and for cloning IL-17 like receptors, using an expression cloning strategy. Radiolabelled or affinity/activity-tagged IL-17 proteins are useful in binding assays to identify a cell type or cell line or tissue that express IL-17 like receptors. A radiolabelled or tagged IL-17 like protein is useful as an affinity ligand to identify and isolate from an expression library the subset of cells which express the IL-17 like receptors on their surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IL-17 like protein, agonist and antagonist are useful for treating acute and chronic inflammation such as rheumatic diseases, graft versus host disease and multiple sclerosis. IL-17 like antagonists are useful for treating and preventing inflammatory disease, autoimmune disease, allergies, asthma and organ or graft rejection in a patient and also proliferation or immunoglobulin secretion, and for blocking the effects of IL-17 in inducing bone destruction. IL-17 like molecule is useful in
                                                                                                                                                                                                                         Human; interleukin, IL-17 like protein; rheumatic disease; gene therapy; multiple sclerosis; graft versus host disease; inflammatory disease; asthma; autoimmune disease; allergy; graft rejection; bone destruction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel interleukin-17 like polypeptides and nucleic acid molecules encoding them useful for diagnosis, prevention and treatment of inflammatory, autoimmune disease, allergies, asthma and organ or graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to interleukin (IL)-17 like polypeptides
drug screening; antlinflammatory; immunosuppressive; antiasthmatic;
neuroprotective; antirheumatic; antiallergic.
                                                                                                                                                                                                                                                                                                                                       5.48
/label= Signal_peptide
49.227
/label= Mature_human_IL-17_like protein
                                                                                                                                                                                                Human interleukin (IL)-17 like protein.
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                        AAE08676 standard; Protein; 227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; Fig 1A; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-FEB-2001; 2001WO-US03916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0180864
2000US-0722920
                                                efihvpvgctcvlprsv 197
                                                                                                                                                                          (first entry)
                                    EFIHVPVGCTCVLPRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-529841/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bass MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD15291
                                                                                                                                                                                                                                                                                                                                                                                                      WO200159120-A2
                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-2000;
27-NOV-2000;
                                                                                                                                                                          15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                               16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rejection
                                                                                                                                                 AAE08676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jing S,
                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                           181
                                   181
                                                                                                            AAE08676
                                                                                                                                     ŏ
                                                           qq
```

```
ö
gene therapy and for mapping the location of the IL-17 like gene and related genes on chromosomes, as hybridisation probes in diagnostic assays. Non-human animals in which the promoter for one or more of IL-17 like protein is either activated or inactivated are useful for drug candidate screening. The present sequence is human IL-17 like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy; multiple sclerosis; graft versus host disease; inflammatory disease; asthma; autoimmune disease; allergy; graft rejection; bone destruction; drug screening; antiinflammatory; immunosuppressive; antiasthmatic; neuroprotective; antirheumatic; antiallergic; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel interleukin-17 like polypeptides and nucleic acid molecules encoding them useful for diagnosis, prevention and treatment of inflammatory, autoimmune disease, allergies, asthma and organ or graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 KLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQ 122
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 92
                                                                                                                                                                                                                                                                                                                                                                            LLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL
                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Wild-type Leu substituted with Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human interleukin (IL)-17 like protein mutant (Leu47Ile).
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                             Score 1063; DB 22;
Pred. No. 6.9e-108;
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE08680 standard; Protein; 227 AA.
                                                                                                                                                                                                                                     99.1%; Scu.
100.0%; Prr
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-FEB-2001; 2001WO-US03916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0180864
2000US-0722920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 ihvpvgctcvlprsv 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 IHVPVGCTCVLPRSV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-529841/58.
                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
                                                                                                                                                                          227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bass MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200159120-A2
```

Location/Qualifiers

```
The present invention relates to interleukin (IL)-17 like polypeptides and nucleic acids encoding them. IL-17 like protein is useful for definity acid partners, agonists and antagonists which can be used for treating one or more diseases or disorders and for cloning IL-17 like receptors, using an expression cloning strategy. Radiolabelled or affinity/activity-tagged IL-17 proteins are useful in binding assays to dentify a cell type or cell incor tissue that express IL-17 like receptors. A radiolabelled or tagged IL-17 like protein is useful as an affinity ligand to identify and isolate from an expression library the subset of cells which express the IL-17 like protein is useful as an affinity ligand to identify and isolate from an expression their surface. IL-17 like protein, agonist and antagonist are useful for treating acute and chronic inflammation such as rheumatic diseases, graft versus host treating and preventing inflammatory disease, autoimmune disease, allerates and organ or graft rejection in a patient and also for inhibiting T cell proliferation and/or activation, in vivo B cell proliferation or immunoglobulin secretion, and for blocking the effects of IL-17 in inducing bone destruction. IL-17 like molecule is useful in gene therapy and for mapping the location of the IL-17 like gene and related genes on chromosomes, as hybridisation probes in diagnostic assays. Non human animals in which the promoter for one or more of IL-17 in the protein mitential the activated or inactivated are useful for drug candidate screening. The present sequence is human IL-17 like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The present sequence is not shown in the specification, but is derived from the human IL-17 like protein referred to as SEQ ID NO:2 (AAE08676), shown in figure 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1061; DB 22; Length 227;
Pred. No. 1.1e-107;
1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE08682 standard; Protein; 227 AA.
  Claim 18; Page -; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.98;
99.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 99.5
nes 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 IHVPVGCTCVLPRSV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE08682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE08682
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

; 0 Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy; multiple sclerosis; graft versus host disease; inflammatory disease; asthma; autoimmune disease; allergy; graft rejection; bone destruction; drug screening; antlinflammatory; immunosuppressive; antiasthmatic; neuroprotective; antirheumatic; antiallergic; mutant; mutein. 123 KLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEF 182 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQ 122 Gaps 33 llpgllfltwlhtciahhdpslrghphshgtphcysaeelplggapphllargakwggal 92 Human interleukin (IL)-17 like protein mutant (Leu47Met).

sapiens Synthetic.

Homo

ö

```
The present invention relates to interfeuent (LL) 'I like propertiaes and nucleic acids encoding them. IL-17 like protein is useful for identifying binding partners, agonists and antagonists which can be used for treating one or more diseases or disorders and for cloning IL-17 like receptors, using an expression cloning strategy. Radiolabelled or affinity/activity-tagged IL-17 proteins are useful in binding assays to identify a cell type or cell line or tissue that express IL-17 like receptors. A radiolabelled or tagged IL-17 like protein is useful as an affinity ligand to identify and isolate from an expression library the subset of cells which express the IL-17 like protein is useful accent. IL-17 like protein, agonist and antagonist are useful for treating and chronic inflammation subset of cals which express the IL-17 like antagonists are useful for treating and preventing inflammatory diseases, autoimmune disease, also many preventing inflammatory disease, autoimmune disease, allergies, asthma and organ or graft rajection in a patient and also for inhibiting T cell proliferation and/or activation, in vivo B cell proliferation or immunoglobulin secretion, and for blocking the effects of IL-17 in inducing bone destruction. IL-17 like molecule is useful in gene therapy and for mapping the location of the IL-17 like gene and consulting in the propertion probes in diagnostic and prove the promosomes, as hybridisation probes in diagnostic and prove the promosomes, as hybridisation probes in diagnostic and prove the promosomes, as hybridisation probes in diagnostic and prove the propertion in the propertion and prove the promosomes, as hybridisation probes in diagnostic and prove the promosomes, as hybridisation probes in diagnostic and prove the propertion in the propertion of the IL-17 in the prope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assays. Non-human animals in which the promoter for one or more of IL-17 like protein is either activated or inactivated are useful for drug candidate screening. The present sequence is human IL-17 like protein mutant (Leu47Net).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel interleukin-17 like polypeptides and nucleic acid molecules encoding them useful for diagnosis, prevention and treatment of inflammatory, autoimmune disease, allergies, asthma and organ or graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention relates to interleukin (IL)-17 like polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The present sequence is not shown in the specification, but is derived from the human IL-17 like protein referred to as SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 227;
                                              /note= "Wild-type Leu substituted with Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1061; DB 22;
Pred. No. 1.1e-107;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page -; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE08676), shown in figure 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.98;
99.58;
                                                                                                                                                                                                          07-FEB-2001; 2001WO-US03916.
                                                                                                                                                                                                                                                              2000US-0180864
                                                                                                                                                                                                                                                                                      27-NOV-2000; 2000US-0722920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-529841/58
                        Misc-difference 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                 Bass MB;
                                                                                                     WO200159120-A2.
                                                                                                                                                                                                                                                              08-FEB-2000;
                                                                                                                                                        16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sednence
                                                                                                                                                                                                                                                                                                                                                                                           Jing S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
```

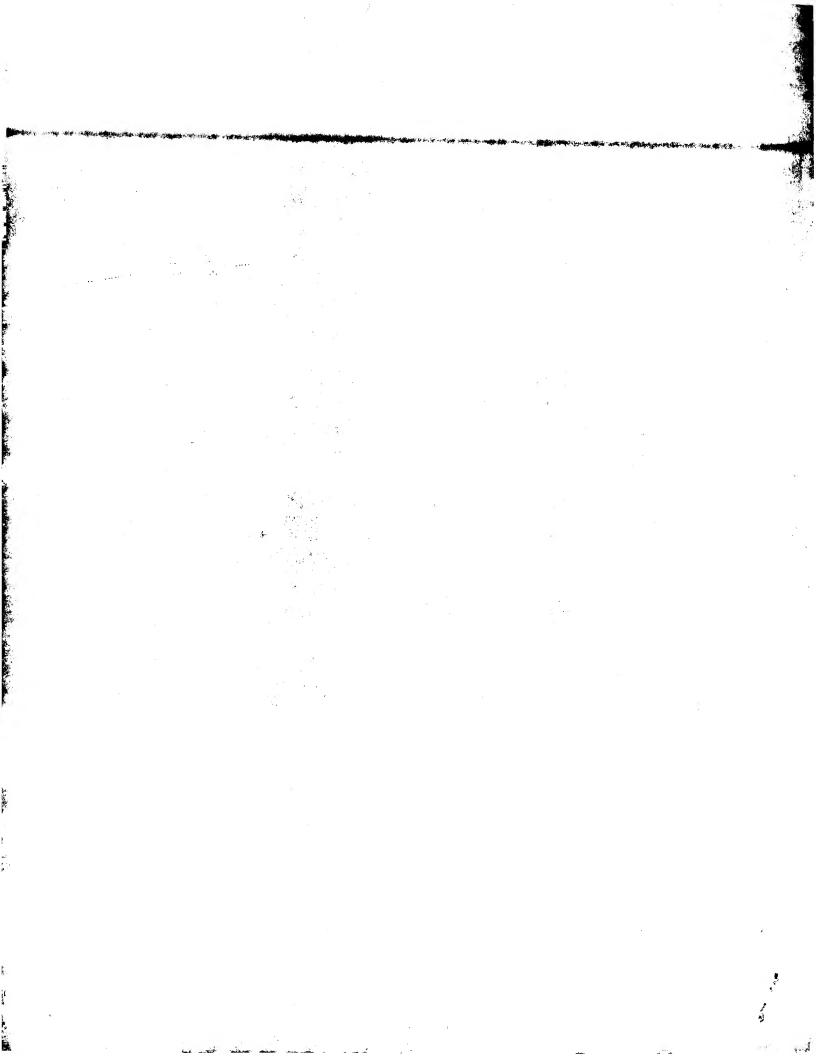
ó g

```
and nucleic acids encoding them. IL-17 like protein is useful for treating one or more diseases or disorders and for cloning IL-17 like receptors, using an expression cloning strategy. Radiolabelled or affinity/activity-tagged IL-17 proteins are useful in binding assays to identify activity-tagged IL-17 proteins are useful in binding assays to identify activity-tagged IL-17 proteins are useful in binding assays to identify a corell type or cell line or tissue that express IL-17 like receptors. A radiolabelled or tagged IL-17 like protein is useful as an affinity ligand to identify and isolate from an expression library the subset of cells which express the IL-17 like receptors on their surface. IL-17 like protein, agonist and antagonist are useful for treating and chronic inflammation such as rheumatic diseases, graft versus host cases and multiple sclerosis. IL-17 like antagonists are useful for treating and preventing inflammation and/or activation, in vivo B cell allergies, asthma and organ or graft rejection in a patient and also for inhibiting T cell proliferation and/or activation, in vivo B cell proliferation between the location of the IL-17 like gene and gene therapy and for mapping the location of the IL-17 like gene and created genes on chromosomes, as hybridisation probes in diagnostic assays. Non-human animals in which the promoter for one or more of IL-17 like assays. Non-human animals in which the promoter for one or more of IL-17 like assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy; multiple sclerosis; graft versus host disease; inflammatory disease; asthma: autoimmue disease; allergy; graft rejection; bone destruction; drug screening; antiinflammatchy; immunosuppressive; antiashmatic; neuroprotective; antirheumatic; antiallergic; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel interleukin-17 like polypeptides and nucleic acid molecules encoding them useful for diagnosis, prevention and treatment of inflammatory, autoimmune disease, allergies, asthma and organ or graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to interleukin (IL)-17 like polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    candidate screening. The present sequence is human IL-17 like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild-type Leu substituted with Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human interleukin (IL)-17 like protein mutant (Leu47Val).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                 AAE08681 standard; Protein; 227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18; Page -; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-FEB-2001; 2001WO-US03916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-NOV-2000; 2000US-0722920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2000; 2000US-0180864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
183 IHVPVGCTCVLPRSV 197
                                        213 ihvpvgctcvlprsv 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001~529841/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Misc-difference 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jing S, Bass MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200159120-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rejection
                                                                                                                                                                                                                                                                                                                                                                                       AAE08681;
                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ношо
                                                                                                                                                                                                                                                             AAE08681
                                                                                                                                                                                                                    RESULT
```

A STATE OF S

```
182
                                                                                                                                                                                                                                                                                     212
          Note: The present sequence is not shown in the specification, but is derived from the human IL-17 like protein referred to as SEQ ID NO:2 (AAEO8676), shown in figure 1A.
                                                                                                                              Gaps
                                                                                                                                                                               92
                                                                                                                                                                                                                                                                          LLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL
                                                                                                                                                                    63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQ
                                                                                                                                                                                                                                                             123 KLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEF
                                                                                                                              ö
                                                                                                    Length 227;
                                                                                                                              Indels
                                                                                                    Score 1060; DB 22;
Pred. No. 1.5e-107;
                                                                                                                              ö
                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Search completed: August 23, 2002, 16:01:48
Job time: 59 sec
                                                                                                    98.8%;
99.5%;
protein mutant (Leu47Val).
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                             183 IHVPVGCTCVLPRSV 197
                                                                                                    Query Match
Best Local Similarity
                                                               AA;
                                                              227
                                                                                                                             Matches 194;
                                                               Sequence
                                                                                                                                                        m
                                                                                                                                                                               셤
                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                     QΩ
2222X8
                                                                                                                                                                                                          Ωy
                                                                                                                                                                                                                                                           Qγ
                                                                                                                                                                                                                                                                                                               δ
```

ö



Query Match:

ŏ a δ a ò g

```
Human; interleukin-22; IL-22; IL-21; immune system disorder;
immune cell chemotaxis; haematopoietic cell disorder;
haemostatic activity; thrombolytic activity; autoimmune disorder; asthma;
respiratory problem; organ rejection; graft-versus-host disease; GVHD;
                                                                                                                             The present sequence is the human PRO1122 polypeptide, also referred to as UNO561, and as interleukin-17C (ILL-17C), encoded by clone DN6237-1381-1. This sequence has identity with the cytokine IL-17 and cytotoxic T-lymphocyte-associated antigen 8 (CTLA-8) and has leucine zipper pattern. PRO1122 is expressed in pancreas, small intestine, stomach and testis also. It shares about 26-28% amino acid identity with IL-17 and IL-17B. The entire coding region of IL-17C can be used as hybridisation probe. The PRO1122 polypeptide, agonist or antagonist, is used to diagnose and treat a degenerative cartilaginous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammation; hyperprolíferative disorder; tissue regeneration; embryonic stem cell differentiation; embryonic stem cell proliferation; haematopoietic lineage; allergic asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 alpvalvssleaashrgrherpsattqcpvlrpeevleadthqrsispwryrvdtdedry 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFTT
                                                                                                                                                                                                                                                                                                                                                                                                                               1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ
                                                  polypeptides designated PRO1031 and PRO1122 used to treat
                                                                                                                                                                                                                                                                                                                                                               Score 1073; DB 21;
Pred. No. 4.6e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "conserved domain VII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "conserved domain VI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of human interleukin-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "conserved domain V"
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note- "signal peptide"
                                                                 degenerative cartilaginous disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY53692 standard; Protein; 197 AA
                                                                                                                                                                                                                                                                                                                                                             100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                   Claim 23; Fig 3; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 EFIHVPVGCTCVLPRSV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "c
113..121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..109
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
104..10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34..40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63..68
WPI; 2000-116314/10.
N-PSDB; AAZ29728.
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 197; Conserv
                                                                                                                                                                                                                                                                                                            197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-2000
                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY53892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
AAY53892
                                                    New
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΣ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interleukin; IL-17C; PRO1122 polypeptide; clone DNA62377-1381-1; UNQ561;
cytokine IL-17; cytotoxic T-lymphocyte-associated antigen 8; CTLA-8;
hybridisation probe; antagonist; degenerative cartilaginous disorder;
                                                                                                                                                                               PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT 180
                                                                                                                                                                                                                                                ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 120
                                                                   Gaps
                                                                                                                              9
                                                                                                9
                                                                                                             MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..18
7.label= Signal_peptide
19..197.
7.label- Mature_IL-17C_polypeptide
7.note= "Used to treat degenerative cartilaginous
                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ž
                                 Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wood
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ή,
                                Score 1073; DB 21;
Pred. No. 4.6e-109;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ľ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Conserved Trp residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Conserved Cys residue'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Conserved Cys residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Conserved Cys residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Interleukin 17C, PR01122 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Conserved Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen J, Filvaroff E, Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Conserved
                                100.0%; Sc
100.0%; Pr
cive 0;
                                                                                                                                                                                                                                                                                                                                                                                                             AAY44460 standard; Protein; 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US10733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0085579.
                                                                                                                                                                                                                                                                                             EFIHVPVGCTCVLPRSV 197
                                                                                                                                                                                                                                                                                                            efihvpvgctcvlprsv 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agonist; diagnose; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder"
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 129
                                               Best Local Similarity
Matches 197; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9960127-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-NOV-1999
```

Peptide Protein

AAY44460;

AAY4460 RESULT

121

181

g ð

121

61

'n

E.

ö

Gaps

ö

Length 197 Indels

9 9

LOHO TO THE

```
The present sequence represents a human interleukin-21 (IL-21)

protein. The specification also describes IL-22 polynuclectides and
polypeptides. The IL-21 polynuclectide was isolated from a cDNA library
of apoptotic T-cells. IL-21 and IL-22 may be useful in treating
deficiencies or disorders of the immune system, by activating or
inhibiting the proliferation, differentiation, or mobilization
(chemotaxis) of immune cells, treating or detecting deficiencies or
disorders of haemacopoletic cells, to modulate haemostatic or
treating asthma (particularly allergic asthma) or other respiratory
problems, to treat and/or prevent organ rejection or graft-versus-host
disease (GVHD), to modulate inflammation, to treat or detect
hyperproliferative disorders, to treat or detect
differentiate, proliferate and attract cells, leading to the
regeneration of itssues, IL-21 may also increase or decrease
the differentiation or proliferation of embryonic stem cells and
harantenericatic lineage, may be used to modulate mammalian
                                                                                                                                                                                                                                                                                                                                                                                                        e.g. immune
                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides used to develop products for treating disorders, blood disorders, autoimmune disorders, allergles, inflammation, hyperproliferative disorders or infections
                                  "conserved domain II"
                                                                           185..192
/note= "conserved domain IV"
 'note= "conserved domain I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 26; Fig 6A-B; 170pp; English.
                                                               "conserved
                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                     98US-0099805.
                                                                                                                                                                                       99WO-US11644
                                                                                                                                                                                                                      98US-0087340
                                             .162
                 129..134
                                  /note=
                                                               /note=
                                                                                                                                                                                                                                                                                                                                               WPI; 2000-072622/06.
                                                                                                                                                                                                                                                                                                                   Ebner R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 197 AA;
                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ36836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 characteristics.
                                                                                                                                                                                                                    29-MAY-1998;
10-SEP-1998;
30-APR-1999;
                                                                                                                         W09961617-A1
                                                                                                                                                                                       27-MAY-1999;
                                                                                                                                                        02-DEC-1999
                                                                                                                                                                                                                                                                                                                 Ruben SM,
                 Domain
                                             Domain
                                                                            Domain
```

```
ö
                                                                                                               ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 120
                                                                                                                                                                       POKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT 180
                                                                                                                                                                                   Gaps
                                                                      1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ
                                                                                                                              ;
0
  100.0%; Score 1073; DB 21; Length 197; 100.0%; Pred. No. 4.6e-109; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                              efihvpvgctcvlprsv 197
                                                                                                                                                                                                                                 EFIHVPVGCTCVLPRSV 197
Query Match 100.
Best Local Similarity 100.
Matches 197; Conservative
                                                                                                                 61
                                                                                                                                                                         121
                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                             181
```

```
The invention relates to novel human proteins designated interleukin (IL)-21 and IL-22. The IL-21 and IL-22 polynucleotides can be used in linkage analysis as a marker for those specific chromosome, in chromosome mapping, to control gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, in identifying individuals from minute biological samples, as an alternative to restriction fragment length polymorphism (RIPLP) analysis, as polymorphism carers for forensic purposes, as molecular weight markers, or as diagnostic probes. IL-21 and IL-22 polypeptides can be used to treat, prevent or diagnose diseases of the immune system by activating or inhibiting the proliferation,
                                                                                                           Interleukin; IL-21; IL-22; immunosuppressive; cytostatic; thrombolytic; antiinfilammatory; antibacterial; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New interleukin-21 and interleukin-22 polynucleotides and polypeptides, useful for treating, preventing or diagnosing e.g. disorders of hematopoietic cells, autoimmune disorders, or hyperproliferative
                                                                                    Human interleukin (IL)-21 amino acid sequence.
                                                                                                                                                                                                                                                                                        104..109
/note= "conserved domain VII"
113..121
                                                                                                                                                                                                                                                                                                                                                                               "conserved domain III"
                                                                                                                                                                                                                                                                           /note= "conserved domain VI"
                                                                                                                                                                                                                                                                                                                                                                                                       "conserved domain IV"
                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                               domain I"
                                                                                                                                                                                                                                                   /note= "conserved domain
                                                                                                                                                                                                /note= "signal peptide"
                                                                                                                                                                                                                          /note= "mature protein"
                                                                                                                                                                           Location/Qualifiers
         AAG66121 standard; Protein; 197 AA.
                                                                                                                                                                                                                                                                                                                             "conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 26; Fig 6A-B; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                        "conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-087340P.
99US-131965P.
99US-169837P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-DEC-2000; 2000US-0731816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US11644
                                                                                                                                                                                                                                                                                                                                                                               /note= "c
185..192
                                                                                                                                                                                                                                                                                                                                           ..134
                                                                                                                                                                                                                                                                                                                                                                    156..162
                                                                                                                                                                                                              19.197
                                                                                                                                                                                                                                        34..40
                                                                                                                                                                                                                                                                 53..68
                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-638470/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ebner R, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EBNER R.
RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAI67878
                                                                                                                                                                                                                                                                                                                                                                                                                             US2001023070-A1.
                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-APR-1999;
09-DEC-1999;
27-MAY-1999;
27-MAY-1999;
                                                           13-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAY-1998
                                    AAG66121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EBNE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases
                                                                                                                                                                                    Peptide
                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                  Domain,
                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                           Domain
AAG66121
```

								, P	F 4 . #	
									Φ.	
										30
MANNEY .	comme de grande es	ang	Market and the second of the second	ng sijihangbertaga — e e specalij	The state of the s	· Y Margarity 11 18	The same of the sa	kito jaga jaga jaga s	i singa	
· ·		٠, ٠								
T.										
); 4										
11										
										1
in the second se										
í										(教 多
i i										
R.										94
<u>.</u>										
r T										
É- -										
					•					
										. 10
										T.
									-	C.
•									,	<i>y</i> .

```
09p795 schizosacch
091gi3 oryza sativ
09144 xanthomonas
09gsz8 cenorhabdi
091783 pseudomonas
                                                                                                                                                                                                  09w4el drosophila
09ulz3 leishmania
096ld4 homo sapien
096h86 homo sapien
086313 mycobacteri
095m4 drosophila
098sj5 brachydanio
                                                                                                                                                                                                                                                                                        09v4d4 drosophila
09u10 drosophila
09xzu7 drosophila
09bwd7 homo sapien
09y4r8 homo sapien
             Q9dps2 meleagrid h
Q9e1h8 meleagrid h
                                                            O9leul arabidopsis
O99391 streptomyce
                                                                                    09j171 mus musculu
09btv9 homo sapien
                                                                                                              Q93zz4 arabidopsis
Q9se51 arabidopsis
                                   Ognyw9 homo sapien
O9y566 homo sapien
 29xdc3 herbaspiril
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li H., Chen J., HubMed=10639155;
MEDLINE=20105548; PubMed=10639155;
Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P., Gurney A.L., Wood W.I.;
Cloning and Characterization of IL-17B and IL17C, Two New Members of the IL-17 Cytokine Family.";
Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).
EMBL; AF152099; AAR-28165.II; -.
CFOUTENCE 197 AA; 21765 MW; BAE0152E18DE7D08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1073; DB 4;
ilarity 100.0%; Pred. No. 2.1e-100;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 AA
                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                Q9LGI3
Q9L4D4
Q9GSZ8
Q9G783
                                                                                                                                                                                                                                                                            Q98SJ5
Q9V4D4
Q9U1I0
Q9XZU7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                           Q9LEU1
Q99391
Q9JL71
                                                                                                           Q93ZZ4
Q9SE51
Q9P795
                                                                                                                                                                                                  Q9W4E1
Q9U123
Q96LD4
Q96H86
Q86313
             Q9DPS2
09E1H8
                                                                                                                                                                                                                                                                                                                             Q9BWD7
Q9Y4R8
Q9BR21
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                    O9NYW9
                                                                                                Q9BTV9
                                                                                                                                                                                                                                                                 Q95RM4
                                                                                                             116 1
113 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9P0M4;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                    ខា
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
Query Match
Best Local Similarity
Matches 197; Conserv
7.77.77.77.77.77.77.77.78.88.88.88.33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERLEUKIN 17C
                                                            86.5
86
86
                                                                                                84.5
84.8
84.8
82.8
81.5
81.5
                                                                                                                                                                                                  8800
800.7799
800.7799
700.7799
700.7799
700.7799
                                                                                                                                                                                                                                                                                                                                                                                                                                                          09P0M4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19
 Q9P0M4
                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                Search time 26.75 Seconds (without alignments) 1274.019 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 saimiriine
6 mesocricetu
bos taurus
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ognue6 homo sapien
Q9eqi7 rattus norv
Q19778 caenorhabdi
Q9beh5 equus cabal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         musculu
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapien
sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9p0m4 homo s
Q9hc75 homo s
Q96pi8 homo s
Q96pd4 homo s
Q99my3 mus m
Q9qxt6 mus m
Q9qxt6 mus m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9cti4 mus m
O40633 saimi
Q9eqi6 mesoc
Q95156 bos ta
Q9uhf5 homo s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                             1 MTLLPGLLFLTWLHTCLAHH......FHTEFIHVPVGCTCVLPRSV
                                                                                                                                                                                                                                                    562222
          4.5
Compugen Ltd.
                                                                                                                                                                                                                                                   Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                         562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
          GenCore version
Copyright (c) 1993 - 2000
                                                                                    August 23, 2002, 16:00:55;
                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9QXT6
Q9H293
Q9CT14
O40633
Q9EL56
Q95L56
Q9UHF5
Q9UUE6
Q9UUE6
Q9EH5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q96PD4
Q99MY3
                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9HC75
Q96PI8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9P0M4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                        sp_fungi:*
sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_archeap:*
                                                                                                                                    US-09-854-208-3
1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
11
11
11
11
11
11
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_plant: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВВ
                                                                                                                                                                                                                                                                                                                                                                   SPTREMBL_19:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197
1197
1163
1180
1180
215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151
178
141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1000.0
99.3
16.11
16.11
15.7
115.7
114.7
114.6
114.6
114.6
114.6
115.7
115.7
116.7
116.8
                                                                                                                                                                                                                                                                                                                                                                                                                     44:
66:
110:
111:
114:
116:
116:
                                                                                                                                                                                                                                                                               sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1073
1065
173
173
168.5
166.5
1160.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
1157.5
                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                      Scoring table:
                                                            OM protein
                                                                                                                                                                                                                                                                            8B
BB
                                                                                                                                                               Sequence:
                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                                                                            Minimum
                                                                                                                                                                                                                                                                                         Maximum
                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
```

ö

Gaps

; 0

~

÷

Gaps

181

ò g

```
97 LEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 LEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLL 156
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=21475830; PubMed=11591732;
Starnes T., Robertson M.J., Sledge G., Kelich S., Nakshatri H.,
Broxmeyer H.E., Hromas R.;
"Cutting Edge: IL-17F, a novel cytokine selectively expressed in activated T cells and monocytes, regulates anglogenesis and endothelial cell cytokine production.";
J. Immunol. 167:4137-4140(2001).
EMBL; AF384857; AAK83350.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11; Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Indels
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang W., Cao X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF25009A AR37427.1; -
SEQUENCE 180 AA; 20268 MW; AAE4CF5FACA3D11E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 AA; 18045 MW; E5287737C9E7BD46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    099MY3;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYTOKINE CXI PRECUSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                           157 VLRRR--PCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                           129 VVRRKHQGCS------VSFQLEKVLVTVGCTCVTP 157
        Pred. No. 5.7e-10;
; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 VLRRR--PCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.1%; Score 173; DB 4; 39.0%; Pred. No. 8.9e-10; iive 16; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                      AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 AA.
                                16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.8%; Score 169.5;
                                                                                                                                                                                                                                                                                                                                                                                                                   163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT:
     39.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, INTERLEUKIN-17F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39; Conservative
Best Local Similarity 39.0 Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                 096PD4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               099MY3
                                                                                                                                                                                                                                                                                                                                                                                                                Q96PD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         വ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
Q99MY3
                                                                                            ò
                                                                                                                                                  g
                                                                                                                                                                                                           QY
                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCOORDER OF THE SECTION OF THE SECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFFFT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
BEDLINE-1475866; PubMed-11591768;
Kawaguchi M., Onuchic L.F., Li X.-D., Essayan D.M., Schroeder J.,
Xiao H.-Q., Liu M.C., Krishnaswamy G., Germino G., Huang S.-K.;
"Identification of a Novel Cytokine, ML-1, and Its Expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutelo
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Zhang W., He L., Wan T., Yuan Z., Cao X.;

"Novel human cytokine Cxz with homology to IL-17.";

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF142410; AAG27921.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21784 MW; BAFBB49F6314A768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Subjects with Asthma.";
J. Immunol. 167:4430-4435(2001).
EMBL; AF332389; AAL14427.1; -.
SEQUENCE 109 AA; 12327 MW; 52C5B34C36DC30EB CRC64;
                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.3%; Score 1065; DB 4; 99.5%; Pred. No. 1.3e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 173; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                     197
                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                  ...maR-2001 (TrEMBLrel. 16, C. 01-MAR-2001 (TrEMBLrel. 16, La CYTOKINE CX2 PRECUSOR. Homo sapiens (Human).

Bukaryota; Metazor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.1%;
                                                           181 EFIHVPVGCTCVLPRSV 197
                             EFIHVPVGCTCVLPRSV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 EFIHVPVGCTCVLPRSV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 EFIHVPVGCTCVLPRSV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 196; Conservative
                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
```

SEQUENCE

Q9HC75;

Q9HC75

RESULT

09HC75

Query Match

ò QQ ò g

g

ò

ð

Query Match

Q96PI8 Q96PI8;

RESULT

096PI8

э;

14; Gaps

 \sim

```
177 AFHTEFIHVPVGCTCV 192
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                        INTERLEUKIN 17E.
                                                                                                                       01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9CTI4;
                                                                                                              09н293;
                                                                                                 09н293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9CTI4
                                                                                                                                                                     IL17E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                            RESULT
                                                                                      09н293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9CTI4
                     ò
                                          a
                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                      LVSSLEAASHRGRHERPSATTQCPVLRPEEVLEAD------THQRSISPWRYRVDTD 116
                                                                                                                                 117 EDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAF 176
                                                                                                                                              01-JUN-2001 (TrEMBLrel. 13, Last sequence update)
CYTOKINE-LIKE PROTEIN ZCYTO7 (NEURONAL INTERLEUKIN-17 RELATED FACTOR)
(INTERLEUKIN 17B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVSSLEAASHRGRHERPSATTQCPVLRPEEVLEAD-----THQRSISPWRYRVDTD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDRYPOKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuronal expression and evaluation as a candidate for the chromosome 5q-linked form of Charcot-Marie-Tooth disease.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLFLTWLHTCLA-HHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVA 65
                                                                ------ 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LLFLTWLHTCLA-HHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVA 65
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
Martinez T., Hoffman R., O'Hara P.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
MOORE E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E.,
Mother D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;
"Identification of a novel IL-17 related factor: Demonstration of
                                                                                                    ||| :: : :||:|| | :: |
LVSRVKPYARMEEYERTLGEMVAQLRNSSEPAKKKCEVNLQLWLSNKRSLSPWGYSINHD
                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 180;
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20309 MW; E26F4C72001997C5 CRC64;
                                                               LLFLLAISIFLAPSHPRNTKGKRKGQGKPS-----PLAPGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82;
         No. 2.2e-09;
matches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.7%; Score 168.5; DB 1
27.0%; Pred. No. 2.8e-09;
                                                                                                                                                                                                                                                              180 AA.
                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28; Mismatches
                                                                                                                                                                                                                                                                                    Created)
          Pred.
                                                                                                                                                                                                                                                             PRT;
AF184970; AAF01319.1; -. AF218726; AAG44135.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC002271; AAH02271.1; -.
                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                               177 AFHTEFIHVPVGCTCV 192
                                                                                                                                                                                                    164 RORVVMETIAVGCTCI 179
                     53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1928397; Ill7b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 53; Conserv
        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                             L17B OR 2CYTO7
                                                                                                                                                                                                                                                            090XT6
                                                                                                                                                                                                                                       9
                                                                                     99
                                                                                                           49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
                   Matches
                                                                                                                                                                                                                                       RESULT
                                          ò
                                                                                    δ
                                                                                                          g
                                                                                                                                   δ
                                                                                                                                                      g
                                                                                                                                                                             õ
                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ob
```

```
MEDLINE=21125711; PubMed=11058597;
Lee J., Ho W.-H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S.,
Lee J., Ho W.-H., Maruoka M., Corpuz R.T., Wood W.I., Gurney A.L.;
Goddard A.D., Yansura D.G., Vandlen R.L., Wood W.I., Gurney A.L.;
"IL-17E, a Novel Proinflammatory Ligand for the IL-17 Receptor Homolog
IL-17RH1";
J. Biol. Chem. 276:1660-1664 (2001).
EMBL, AR305200; AA64084848.1;
SEQUENCE I77 AA; 20330 MW; 52D895710CD59871 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SERAIN-C57BL/6J; TISSUB-EMBRYO;
STRAIN-C57BL/6J; TISSUB-EMBRYO;
STRAIN-C57BL/6J; TISSUB-EMBRYO;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Kadota K., Matsuda H.A., Nikaido I., Fesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 PSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 HPHSHGTPHCYS----AEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHER 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 HTYSHWPSCCPSKGQDTSEEL-----LRW-STVP---VPPLEPARPNRHPES
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 ETAAL-NSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 HMDPRGNSELLYHNQTVFYRRPCHGEKG---THKGYCLERRLYRVSLACVCVRPR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1110006016RIK PROTEIN (FRAGMENT).
ILI7B OR 1110006016RIK.
                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 165.5; DB 4;
Pred. No. 5.5e-09;
6. Wismatches 70;
                                                                                                                                                                                    177 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Mismatches
                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                  (TrEMBLrel. 16, C
(TrEMBLrel. 16, I
(TrEMBLrel. 19, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.4%;
29.7%;
: |||||:
164 RQRVVMETIAVGCTCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
```

7;

```
156 LVLRR--RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                         O9EQI6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          095156
                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         095156
              ò
                                                                         g
                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ر
ر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ς;
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Massliman M., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Waynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : :::||:||| | :: | | | | | | | || ||: | :: | :: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : | | | | | : | : | | | | : | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 RPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 GQRRPSPLAPGP---HQVPLDLVSRVKPYARMEEYERNLGEMVAQLRNISEPAKKKCEV- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knappe A., Hiller C., Thurau M., Wittmann S., Hofmann H.,
Fleckenstein B., Fickenscher H.;
"The superantigen-homologous viral immediate-early gene iel4/vsag in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PSATTQCPVL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AKO03506; BAB2286-1; -.
MGD; MGI:1928397; Il17b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 14.7%; Score 157.5; DB 12; Length 151; Best Local Similarity 28.6%; Pred. No. 3e-08; Matches 46; Conservative 22; Mismatches 58; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 AA; 24196 MW; 21468E7E01A92154 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49B2C9430C46BE32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 LQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2e-08;
les 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.0%; Score 160.5;
29.8%; Pred. No. 2.2e
iive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 GQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHER-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98037620; PubMed-9371569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 15.0
Best Local Similarity 29.8
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saimiriine herpesvirus 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
INTERLEUKIN 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               040633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          040633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      040633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
```

```
45 GQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEAD---- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 LQLWLSNKRSLSPWGYSINHDPSRIPADLPEARCLCLGCVNPFTMQEDRSMVSVPVF-SQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 -----THQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuronal expression and evaluation as a candidate for the chromosome 5q-linked form of Charcot-Marie-Tooth disease."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF10155; AAG44134.1; ...
NON TER 178 178
SEQUENCE 178 AA; 20071 MW; 03D02D60BEC89A51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 GOVRPGPLAPGP---HQVPLDLVSRVKPYARMEEYERNLGEMVAQLRNSSEPAKRRCEVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MORONAL INTERLEUKIN-17 RELATED FOCTOR (FRAGMENT).
MESOCRICETUS auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E., Moore E.E., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.; "Identification of a novel IL-17 related factor: Demonstration of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.7%; Score 157.5; DB 11; Length 178; 29.5%; Pred. No. 3.6e-08; ive 23; Mismatches 70; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee I.-K., Mwangi S.M., Olsen S., Kehrli M. Jr.,
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF416586; AAL08013.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERLEUKIN 17.
94077A79DD803F3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
----SFRLEKMLVTVGCTCVTP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 LVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 VPVRRRLCPPP----PRPGPCRHRVVMETIAVGCTC 178
                                                                                                                                              178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.6%; Score 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141
15945 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, INTERLEUKIN 17 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos.
116 LVVRKGHNPCPN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               Mesocricetus.
NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
```

4;

.,

```
20437 MW; F1B0BC1446D0B14A CRC64;
                                                                        45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
     180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NERF (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
     SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  DJ108C2.3
                                                                                                                                                                                                                                                                                                        OBNUE6
                                                                                                                                                                                                                                                                                                                      O9NUE6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09EQI7
                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54
                                                                                                                                                                                                                                                                                           09NUE6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OBEOI.
     SO
                                                                                                 ŏ
                                                                                                                         g
                                                                                                                                                       ò
                                                                                                                                                                                 g
                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                      рp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC
DT
DT
DT
DT
DT
OC
OC
OC
OC
OC
NX
RP
RP
RP
RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.L., Yi Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20105548; PubMed-10639155;
Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,
Gurney A.L., Wood W.I.;
"Cloning and Characterization of IL-17B and IL17C, Two New Members of
the IL-17 Cytokine Femily.";
Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).
                                           DTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLR 159
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moore E.E., Present S., Garrigues U., Guilbot A., LeGuern E., Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.; "Identification of a novel IL-17 related factor: Demonstration of neuronal expression and evaluation as a candidate for the chromosome Sq-linked form of Charcot-Marie-Tooth disease."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J., Martinez T., Hoffman R., O'Hara P.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20317118; PubMed=10749887;
Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski K.J.,
Barber M.C., Wang W., Wathen K., Hodge V., Fisher C.L., Olsen H.,
Ruben S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A.,
Carrell J.A., Ebner R.;
A novel oytokine receptor-ligand pair. Identification, molecular
characterization, and in vivo immunomodulatory activity.";
J. Biol. Chem. 275:19167-19176(2000).
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYTOKINE-LIKE PROTEIN ZCYTO? (INTERLEUKIN 20) (INTERLEUKIN 17B)
(NEURONAL INTERLEUKIN-17 RELATED FACTOR) (INTERLEUKIN-17 BETA).
ZCYTO? OR IL20 OR IL17B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel Nickerson D.A.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang W., Wang J., Cao X.;
"Novel cytokine homology with interleukin-17.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
     Pred. No. 3.1e-08;
                                                                                                              160 RRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
40.0%; Preu. ....
                                                                                                                                                                                             180 AA.
                                                                                                                                                                                                         Q9UHF5;
01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF184969; AAF01318.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF212311; AAF78775.1;
AF152098; AAF28104.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF218727; AAG44136.1;
EMBL; AF110385; AAG39637.1;
EMBL; AF386077; AAK60336.1;
                 Conservative
                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                            Q9UHF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                  RESULT 12
                                                                                                                         110
                                          100
                                                                    51
                 Matches
                                                                                                                                                                               09UHF5
                                           ò
                                                                                              ò
                                                                                                                         a
                                                                                                                                                                                               g
```

```
45 GQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEAD---- 100
                                                                                                                                                                                             101 ----THORSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 VDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRR--PCSRDGSGL 170
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DJ108C2.3 (PUTATIVE NOVEL PROFIEIN SIMILAR TO ILL) (INTERLEUKIN 17
(CYTOTOXIC T-LYMRHOCYTE-ASSOCIATED SERINE ESTERASE 8)) (CYTOTOXIC
DLYMPHOCYTE-ASSOCIATED ANTIGEN 8, CTLA8)) (FRAGMENT)
                                                                                                                                                                                                                         88 LQLWMSNKRSLSPWGYSINHDPSRIPVDLPEARCLCLGCVNPFTMQEDRSMVSVPVF-SQ
                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
  Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E. Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Indels
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Almeida J.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66C3C34E7ACC2790 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                   70;
       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 136; DB 4;
Pred. No. 2.1e-06;
  Score 154.5; DB 4
Pred. No. 7.3e-08;
                                                                                                                                                                                                                                                                                         156 LVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCV 192
                                                                                                                                                                                                                                                                                                                                     147 VPVRRRLCPPP----PRTGPCRORAVMETIAVGCTCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 PTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
14.48;
28.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.7%;
39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 AA; 8704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16,
16,
16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL034343; CAB75300.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15,
```

.; Э

Ç

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
"Identification of a novel IL-17 related factor: Demonstration of neuronal expression and evaluation as a candidate for the chromosome 5q-11nked form of Charcot-Marie-Trooth disease.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF218724; AAG44133.1; -.
NON_TER 1 1 1 11
SEQUENCE 111 AA; 12628 MW; D1598392981BA867 CRC64;
                                                                                                                                                                                                                                             101 THORSISPWRYRVDTDEDRYPOKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 ORSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRP 162
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                30 SNKRSLSPWGYSINHDPSKIPEDLPEARCLCLGCVNPFTWQEDRSMVSVPVF-SQVPVRR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                             2;
                                                                                                                                                                         Query Match
Best Local Similarity 37.8%; Pred. No. 1.4e-05;
Matches 28; Conservative 16; Mismatches 25; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 10.3%; Score 110; DB 5; Length 148; Best Local Similarity 33.0%; Pred. No. 0.0018; Matches 31; Conservative 17; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kelly P.F.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                investigating biology.";
Science 282:2012-2018[1998].
EMBL: 273973; CAR9826811; -.
SEQUENCE 148 AA; 16738 MW; ADB51F438DFB3940 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F25D1.3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 CSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPRS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 CDR-STGL---WNYVRSTELI--TVGCHSVLPRT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: August 23, 2002, 16:03:07 Job time: 132 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-99069613; Pubmed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                               161 RPCSRDGSGLPTPG 174
                                                                                                                                                                                                                                                                                                                                    | | : | 1|
89 RLCPQP----PRPG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q19778
Q19778;
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                   019778
     g
                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

us-09-854-208-3.rsp

```
August 23, 2002, 16:00:55; Search time 11.96 Seconds (without alignments) 637.772 Million cell updates/sec
                                                                                                                                                                                              US-09-854-208-3
1073
1 MTLIPGLLFLTWLHTCLAHH.....FHTEFIHVPVGCTCVLPRSV 197
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                            105224 seqs, 38719550 residues
                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                 Run on:
```

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9p0m4 homo sapien	homo	mus n	hom	herpe			Q9eqi6 mesocricetu	Q9uhf5 homo sapien		Q62386 mus musculu	Q9ubc0 homo sapien	-		P25439 drosophila	Q55694 synechocyst	P20268 caenorhabdi			Q15650 homo sapien	sacch	Q09013 homo sapien	homo	P21709 homo sapien	P70478 rattus norv	Q03365 sus scrofa		P95114 mycobacteri	gallus	gallus	h nucl	escher	Q9myv3 canis famil
SUMMARIES	ΙD	117C_HUMAN	117F_HUMAN	117B_MOUSE	I17E_HUMAN	VG13_HSVSA	IL17_HUMAN	VG13_HSVSC	I17B_MESAU	I17B_HUMAN	IL17_RAT	IL17_MOUSE	HNF6_HUMAN	HNF6_MOUSE	HNF6_RAT	BRM_DROME	GIDA_SYNY3	HM06_CAEEL	FAST_HUMAN	FRA2_CHICK	TRI4_HUMAN	PR19_YEAST	DMK_HUMAN	TNR7_HUMAN	EPA1_HUMAN	APC_RAT	HNFB_PIG	NFL1_MOUSE	DDL_MYCTU	GAT2_CHICK	CP15_CHICK	NFL1_HUMAN	COBC_ECOLI	VEGA_CANFA
	DB	1																			7													
	Length	197	153	180	177	151	155	151	178	180	150	158	465	465	465	1638	635	325	549	323	581	503	639	260	916	2842	559	741	373	466	528	772	203	214
	% Query Match	0	16.1	15.7	S	S	**	4	₹.	₹.	•	٠	•		•	7.9	•	•	٠		7.2	٠		•	•	٠	•	٠	•	9.8	•	٠	6.7	6.7
,	Score	1073	173	168.5	165.5	160.5	158	157.5	157.5	154.5	148.5					84.5			\sim		77.5		74.5	74	74	7	73.5	m.	73				71.5	71.5
	Result No.	1	7	m	4	2	9	7	80	o	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

ó;

Gaps

; 0

Length 197; Indels 1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60

δλ

Ouery Match 100.0%; Score 1073; DB 1; Best Local Similarity 100.0%; Pred. No. 5.4e-94; Matches 197; Conservative 0; Mismatches 0;

P31258 gallus gall Q47474 erwinia chr P23050 avian retro P54977 streptomyce P11939 gallus gall Q9h254 homo sapien Q9yfp5 acropyrum p P31311 mus musculu Q9es28 mus musculu Q9es28 mus musculu P49908 homo sapien P50901 branchiosto Q9y218 homo sapien	S.). Chordata; Craniata: Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.	in.A. 1548; PubMed=10639155; 1., Huang A., Stinson J., Heldens S., Foster J., Dowd P., Wood W.I.; characterization of IL-17B and IL-17C, two new members cytckine family."; cyd. Sci. U.S.A. 97:773-778(2000).	[2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM W., He L., Wan T., Yuan Z., Cao X.; Novel human cytokine CX2 with homology to IL-17."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).	OTENTIAL. SIMILARITY. SIMILARITY. SIMILARITY> R (IN REF. 2). BAE0152E18DE7D08 CRC64;
CHICK AVINK AVINK STRGR CHICK LHUMAN ABRPE MOUSE MOUSE HUMAN BRAFI BRAFI LHUMAN	ALIGNMENTS	upda on up (Cyto	ata; rhini	., не -17В 3-778	ao X 10gy nBan) e of cell	It information in the state of	POTENTIAL. INTERLEGKIN-17C BY SIMILARITY. BY SIMILARITY. H -> R (IN REF. BAE0152E18DE7
HXAB_CHICK PMEB_ERWCH CRTB_STRGR FOS_AVINK CRTB_STRGR FOS_CHUMAN KPTA_AERPE HXAB_MOUSE PIXB_MOUSE SELP_HUMAN HOX3_BRAFL ZF95_HUMAN	ALIG PRT:	ence tati 7C)	rani atar	55; on J f IL 7:77	., c homo L/Ge leas ytic ted. IL-1	ght. Bio titu ns a not eeme	TENT TERL SIM SIM SIM
HXAB_ FOS_A CRTB_ FOS_C SPCO_ SPCO_ HXAB_ PIXB_ SELP_ HOXB_ ACES_	Δ	ed) sequ anno IL-1	a;;	6391 tins on o A. 9	an Z ith EMB e re onoc ecre	pyrippyrice of Institution is agr	POO' IN' BBY BBY H
лпппппппппппппппппппппппппппппппппппппп		eat ist ist or (dat	=10 , S .ati	Yu 12 w 12 w 14 he 14 th 16 m 17 S	co tut ics itit ent ent ent	. 1; . 1;
294 3423 3422 2564 2564 313 313 4111 831	STANDARD:	. 41, Created) . 41, Last sequ . 41, Last anno precursor (IL-1	n). ;; Chor ;; Prim	PubMed ang A. W.I.; cteriz ine fa Sci. U	dan T., ine CX 19) to ulates rom th	try is institution in the instit	AAF28105.1 AAG27921.1 18 197 191 50 A; 21765
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	ATS	(Rel. (Rel. (Rel. (Rel.	(Huma Metazoa utheria 9606;	OM N.A. J., Hu Wood I chara Cytok Acad.	N N.A. E L., W L., W APR-199 N: Stim Libeta L JLAR LC	PROT en Swiss Swiss Bioin Profi I this Huires	(199; AA); (199; AA); (190; AA); (190; AB); (190; AB); (190; AA);
71.5 71.5 71 71 70.5 70.5 70.5	RESULT 1 117C_HUMAN 1D 117C HUMAN	09P0M4; 09HC75; 01-MAR-2002 (Rel. 41, Creat 01-MAR-2002 (Rel. 41, Last 01-MAR-2002 (Rel. 41, Last Interleukin-17C precursor (	1617C. Homo sapiens (Human). Eukaryota; Metazoa; Cl Mammalia; Eutheria; P. NCBI_TaxID=9606;	[1] SEQUENCE FROM N.A. MEDLINE=20105548; PubMed=10639155; Li H., Chen J., Huang A., Stinson J., Heldens S. Gurney A.L., Wood W.I.; "Cloning and characterization of IL-178 and IL-: of the IL-17 cytokine family."; Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).	2) EQUENCE FRC hang W., He Novel human ubmitted (P - FUNCTION and IL-1 - SUBCELLU	his SWISS-I he Europear se by non odified and ntities req	EMBL; AF152099; AAF28105.1; EMBL; AF142410; AAG27921.1; MIN; 604628; SIGNAL CHAIN DISULFID DISULFID CONFLICT SONFLICT
888888444448888888444448888888	SULT 7C_H						
	RES 11	AC DI	<b>3</b> 8 8 8 8	RA RA RA RT RT	R R R R P P P P P P P P P P P P P P P P	388888888	DRA

```
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                   117B_MOUSE
 QQ
                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Funnedial J. Cai L., Risser P., Maruoka M., Mao W., Foster J., Kelley R.F., Pan G., Gurney A.L., Maruoka M., Mao W., Foster J., Kelley R.F., Pan G., Gurney A.L., Starovasnik M.A.;

de Vos A.M., Starovasnik M.A.;

"IL-17s adopt a cystine knot fold: structure and activity of a novel cytokine, IL-17F, and implications for receptor binding.";

EMBO J. 20:5332-5341 (2001).

- I. FUNCTION: Stimulates the production of other cytokines such as IL-

6, IL-8 and granulocyte colony-stimulating factor, and can regulate cartilage matrix turnover. Stimulates PBMC and T-cell proliferation. Inhibits anglogenesis.
                                                                                                  121 PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 but not resting, CD4+
             9
                                                                                                                                                                                                                       Broxmeyer H.E., Hromas R.; "IL-17F, a novel cytokine selectively expressed in activated T cells and monocytes, regulates anglogenesis and endothelial cell cytokine
ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY
                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 2-153 FROM N.A.
MEDLINE=21475866; PubMed=11591768;
Memaguchi M., Onuchic L.F., Li X.-D., Essayan D.M., Schroeder J.,
Xiao H.-Q., Liu M.C., Krishnaswamy G., Germino G., Huang S.-K.;
"Identification of a novel cytokine, ML-1, and its expression in
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-21475830; Pubmed-11591732; Starnes T., Robertson M.J., Sledge G., Kelich S., Nakshatri H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS), AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: Expressed in activated,
-i- Cells and activated monocytes.
-i- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunol. 167:4137-4140(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunol. 167:4430-4435(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 76-153 FROM N.A.
                                                                                                                                    181 EFIHVPVGCTCVLPRSV 197
                                                                                                                                                 181 EFIHVPVGCTCVLPRSV 197
                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subjects with asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed~11574464;
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                             production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Almeida
                                     61
                                                                                                                                                                                                             117F_HUMAN
                                                                                                                                                                                                                         op
                                                            요
                                                                                   ò
                                                                                                            g
                                                                                                                                    ò
                                     ò
```

```
<u>ښ</u>
noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 LEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moore E.E., Presentl S., Garrigues U., Guilbot A., LeGuern E., Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.; "Identification of a novel IL-17 related factor: demonstration of neuronal expression and evaluation as a candidate for the chromosome Sq-linked form of Charcot-Marie-Tooth disease."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lehner J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117B_MOUSE STANDARD; PRT; 180 AA.
090XT6; 099MX3; 09CTT4;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
(Nervin'17B precursor (IL-17B), (Cytokine-like protein ZCYTO7)
(Neuronal interleukin-17 related factor) (Cytokine CX1).
IL17B OR ZCYTO7 OR NIRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Presnell S., Gilbert T., Whitmore T., Foster D., Hart C.,
Martinez T., Hoffman R., O'Hara P.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang W., Cao X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (WITH C-37').
BB489BED883D57CE CRC64;
                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .).
INTERCHAIN (WITH C-127').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 VLRRR--PCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.1%; Score 173; DB 1; 39.0%; Pred. No. 1.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 VVRRKHQGCS------VSFQLEKVLVTVGCTCVTP
                                                                                                                                                                                                                                  Cytokine; Glycoprotein; Signal; 3D-structure. SIGNAL
                                                                                                                                                                                                                                                                                           POTENTIAL.
INTERLEUKIN-17F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Mismatches
modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                              EMBL; AF384857; AAK83350.1; ALT_INIT
EMBL; AF332389; AAL14427.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17009 MW;
                                                                                                                                                                            EMBL; AL034343; CAB75300.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BALB/C;
                                                                                                                                                                                                          MIM; 606496;
                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
R Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washlo T.,
Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Manhabarts P.,
Lyons P., Marchionni L., Mashima J., Manhabarts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVSSLEAASHRGRHERPSATTQCPVLRPEEVLEAD------THQRSISPWRYRVDTD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 LVSRVKPYARMEEYERNLGEMVAQLRNSSEPAKKKCEVNLQLMLSNKRSLSPWGYSINHD 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 EDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSRIPADLPEARCLCLGCVNPFTMQEDRSMVSVPVF-SQVPVRRRLCPQP----PRPGPC 163
                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Stimulates the release of tumor necrosis factor alpha and IL-IDeta from the monocytic cell line THP-1 (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 LLFLTWLHTCLA-HHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 LLFLLAISIFLAPSHPRNTKGKRKGQGRPS-----PLAPGP------HQVPLD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERLEUKIN-17B.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
MDWPHSL -> YPTSTFS (IN REF. 4).
G -> R (IN REF. 4).
R -> K (IN REF. 3).
N -> I (IN REF. 3).
S -> I (IN REF. 3).
K -> K (IN REF. 3).
K -> K (IN REF. 3).
K -> K (IN REF. 3).
K -> I (IN REF. 4).
                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.7%; Score 168.5; DB 1
Best Local Similarity 27.0%; Pred. No. 5.5e-09;
Matches 53; Conservative 28; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF184970; AAF01319.1; -.
EMBL; AF218726; AAG44135.1; -.
EMBL; AF250308; AAK37427.1; -.
EMBL; AK003506; BAB22826.1; -.
EMBL; BC002271; AAH02271.1; -.
MGD; MGI:1928397; Il17b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytokine; Glycoprotein; Signal SIGNAL 1 22 Pt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20309 MW;
                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 AFHTEFIHVPVGCTCV 192
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109
      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

164 RORVVMETIAVGCTCI 179

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-21125711; PubMed=11058597;
Lee J., Ho W.-H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S.,
Leedrd A.D., Yansura D.G., Vandlen R.L., Wood W.I., Gurney A.L.;
"IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog
IL-17Rhl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 CRASEDGPL------NSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 PSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 HPHSHGTPHCYS----AEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHER 81
                                                                                                                                                                                                                                                                                                                                                                                       -i. TISSUE SPECIFICITY: Expressed at low levels in several tissues, including brain, kidney, lung, prostate, testis, spinal cord, adrenal gland, and trachea.
-i. SIMILARITY: BELONGS TO THE IL-17 FAMILY.
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 ETAAL-NSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 HMDPRGNSELLYHNQTVFYRRPCHGEKG---THKGYCLERRLYRVSLACVCVRPR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.4%; Score 165.5; DB 1; Length 177; 29.7%; Pred. No. 1e-08;
                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 276:1660-1664(2001).
-!- FUNCTION: Induces activation of NF-kappaB and stimulates production of the proinflammatory chemokine IL-8.
-!- SUBCELLUIAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
N-LINKED (GLCNAC. . .) (PG
52D895710CD59871 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70;
                                                           (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERLEUKIN-17E.
                              177 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                             PRT;
                                                                                                             Interleukin-17E precursor (IL-17E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 PC
177 IN
168 BY
170 BY
136 N-
20330 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequ
01-MAR-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytokine; Glycoprotein; Signal SIGNAL 1 32 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF305200; AAG40848.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Conservative
                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33
110
115
136
17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                           01-MAR-2002 (
01-MAR-2002 (
01-MAR-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             605658;
                             117E_HUMAN
Q9H293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VG13_HSVSA
P24916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
```

```
Best Loca
Matches
                                  qq
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ---- DYYNRSTSPWTLHRNEDQDRYPSVIWEAKCRYLGCVNA-DGNVDYHMNSVPIQQEI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
                                                                                     MEDLINE-90163221; PubMed-2154888;
Albrecht J.-C., Fleckenstein B.;
"Structural organization of the conserved gene block of Herpesvirus
saimiri coding for DNA polymerase, glycoprotein B, and major DNA
                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=92333688; PubMed=1321287;
Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
Honess R.W.;
                                                                                                                                                                                                                                                                               18 CIVKSEITSAQTPRCLAA----NNSFPRSVMVTLSIRNWNTSSKRAS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
53BEDDE4206C6432 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
IMMEDIATE EARLY GENE 13 PROTEIN.
SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                          "Primary structure of the herpesvirus saimiri genome.";
J. Virol. 66:5047-5058(1992).
                                Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 LVVRKGHQPCPN-----SFRLEKMLVTVGCTCVTP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 LVLRR--RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.0%; Score 160.5; DB 1 ilarity 28.6%; Pred. No. 2.6e-08; Conservative 23; Mismatches 57
 Immediate early gene 13 protein precursor
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-91021021; PubMed-1699352;
          13 OR KCLF2.
Herpesvirus saimiri (strain 11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X64346; CAA45636.1; -. EMBL; M31122; AAA46169.1; -. EMBL; M60286; AAA46156.1; -. PIR; D36807; B45351; B45351; B45351;
                                                                                                                                   binding protein.";
Virology 174:533-542(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17180
                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                       NCBI_TaxID-10383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytokine; Early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96281911; PubMed=8676080;
Fossiez F., Djossou O., Chomarat P., Flores-Romo L., Ait-Yahia S.,
Maat C., Pin J.-J., Garrone P., Garcia E., Saeland S., Blanchard D.,
Gaillard C., Das Mahapatra B., Rouvier E., Golstein P., Banchereau J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- DATABASE: NAME-R&D Systems' cytokine mini-reviews: IL17;
WWW-"http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=211".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 ADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND HEMATOPOIETIC CYTOKINES. ENHANCES THE SURFACE EXPRESSION OF THE INTRACELLULAR ADHESION MOLECULE-1 (ICAM-1) IN FIBROBLASTS.
                                                                                      01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Interleukin-17 precursor (IL-17) (IL-17A) (Cytotoxic T lymphocyte-
associated antigen 8) (CTLA-8).
                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINKED (GLCNAC. . .) (POTENTIAL).
2BCAE9CB2F4886D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: HOMODIMER.
-!- SUBCELLULAR LOCATION: Secreted.
-! TISSUE SPECIFICITY: RESTRICTED TO ACTIVATED MEMORY T-CELLS.
-!- PTM: FOUND BOTH IN GLYCOSYLATED AND NONGLYCOSYLATED FORMS.
-!- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.7%; Score 158; DB 1; Length 155; 39.8%; Pred. No. 4.5e-08; ive 11; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yao Z., Painter S.L., Fanslow W.C., Ulrich D., Macduff B.M. Spridgs M.K., Armitage R.J.;
"Human IL-17: a novel cytokine derived from T cells.";
J. Immunol. 155:5483-5486(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "T ceil interleukin-17 induces stromal cells to produce proinflammatory and hematopoietic cytokines."; J. Exp. Med. 183:2593-2603(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 RRRP--CSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERLEUKIN-17.
      155 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=T-cell;
MEDLINE=96094436; PubMed=7499828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 603149; -.
Cytokine; Glycoprotein; T-cell;
                                                            01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68
17504 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z58820; CAA91233.1; -. EMBL; U32659; AAC50341.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                               IL17 OR IL17A OR CTLA8.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 1
94 1
99 1
68
155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 39; Conserv
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lebecque S.;
IL17_HUMAN
Q16552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
```

'n

```
.9e-08;
                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 VPVRRRLCPPP----PRPGPCRHRVVMETIAVGCTC 178
                                                                                                                                                                                                                                                                                                                                                                INTERLEUKIN-17B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 LVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.7%; Score 157.5; 29.5%; Pred. No. 5.9
                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
              Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                             23
23
75 > 178
75 175
1 176 L
178 L
                                                                                                                                                                                                                                                                                                                           EMBL; AF218725; AAG44134.1; -. Cytokine; Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                              23 >1
75
121 1
126 1
178 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                   SEQUENCE FROM N.A.
                                                           NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                 Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I17B_HUMAN
Q9UHF5;
                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117B_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ДQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ----DYYNRSTSPWTLYRNEDQDRYPSVIWEAKCRYLGCVNA-DGNVDYHMNSVPIOOEI 115
                                                                                                                                                                                                                                                  "The superantigen-homologous viral immediate-early gene ie14/vsag in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Interleukin-17B precursor (IL-17B) (Neuronal interleukin-17 related factor) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 CIVKSEITSAQTPRCLAA----NNSFPRSVMVTLSIRNWNTSSKRAS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL. IMMEDIATE EARLY GENE 13 PROTEIN.
                                                                                                                                                                                                              MEDLINE-98037620; PubMed-9371569;
Knappe A., Hiller C., Thurau M., Wittmann S., Hofmann H.,
Fleckenstein B., Fickenscher H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49B2C9430C46BE32 CRC64;
                                                                                                                                          Herpesvirus saimiri (subgroup C / strain.488),
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.7%; Score 157.5; DB 1;
28.6%; Pred. No. 4.9e-08;
Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 LVLRR--RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                             123 RREPPHCPN-----SFRLEKILVSVGCTCVTP 149
                                                                              01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Immediate early gene 13 protein precursor.
                                                           151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine; Early protein; Signal.
SIGNAL 1 22 POI
                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
140
142
162
36
83
N
64
N
17189 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y13183; CAA73627.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 28.64
Matches 46; Conservative
                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
90
95
36
36
53
64
151 AA;
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                            NCBI_TaxID=10384;
                                                         VG13_HSVSC
O40633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117B_MESAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9EQ16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                            VG13_HSVSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I17B_MESAU
                                 RESULT
8
                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 LQLWLSNKRSLSPWGYSINHDPSRIPADLPEARCLCLGCVNPFTWQEDRSWVSVPVF-SQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 GQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEAD---- 100
                                                                                                                                                                             Moore E.E., Pressell S., Garrigues U., Guilbot A., LeGuern E., Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.; "Identification of a novel IL-17 related factor: demonstration of neuronal expression and evaluation as a candidate for the chromosome 5q-linked form of Charcot-Marie-Tooth disease."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Stimulates the release of tumor necrosis factor alpha and IL-labet from the monocytic cell line THP-1 (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 ----THQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 GOVRPGPLAPGP---HOVPLDLVSRVKPYARMEEYERNLGEMVAQLRNSSEPAKRRCEVN 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
Martinez T., Hoffman R., O'Hara P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Interleukin-17B precursor (IL-17B) (Cytokine-like protein ZCYTO7)
(Neuronal interleukin-17 related factor) (Interleukin-20).
IL17B OR ZCYTO7 OR NIRF OR IL20
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      · · · ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03D02D60BEC89A51 CRC64;
```

۲,

```
10
                                                                          0.1
                                                                                                                                                                                                                                                                  IL17_RAT
                                                                                                                                                                                                                                                RESULT
                                       qq
                                                                                                               g
                                                                            ò
                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q., Mickerson D.A.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Stimulates the release of tumor necrosis factor alpha and IL-1beta from the monocytic cell line THP-1.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed in adult pancreas, small intestine, stomach, spinal cord and testis. Less pronounced expression in prostate, colon mucosal lining, and ovary.
-!- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
                                                                                                                                                                                                                     SEQUENCE FROM N.A. WELLINE-20105548.
MEDLINE-20105548; Pubmed=10639155;
Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P., Gurney A.L., Wood W.I.;
"Cloning and characterization of IL-17B and IL-17C, two new members
                                                                                                                                                                                                                                                                                                                                                                                           Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E., Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.; "Identification of a novel IL-17 related factor: demonstration of neuronal expression and evaluation as a candidate for the chromosome 5q-linked form of Charcot-Marie-Tooth disease."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                             SEQUENCE FROM N.A.
MEDLINE-20317118; Pubmed-10749887;
Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski K.J.,
Barber M.C., Wang W., Wathen K., Hodge V., Fisher C.L., Olsen H.,
Ruben S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A.,
                                                                                                                           Carrell J.A., Ebner R.;
"A novel cytokine receptor-ligand pair. Identification, molecular characterization, and in vivo immunomodulatory activity.";
J. BJOI. Chem. 275:1916(7-19176(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL). F1B0BC1446D0B14A CRC64;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang W., Wang J., Cao X.;
"Novel cytokine homology with interleukin-17.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                    of the IL-17 cytokine family.";
Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERLEUKIN-17B.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY. SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AF184969; AAF01318.1; --
EMBL, AF212311; AAF7875.1; --
EMBL, AF152098; AAF28104.1; --
EMBL, AF210372; AAG44136.1; --
EMBL, AF110385; AAG39637.1; --
EMBL, AF386077; AAK60336.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytokine; Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20437 MW:
Submitted (SEP-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     604627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                   of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
```

4;

Gaps

17;

14.4%; Score 154.5; DB 1; Length 180; 28.7%; Pred. No. 1.1e-07; ive 25; Mismatches 70; Indels 17

Conservative

Ouery Match Best Local Similarity Matches 45; Conserv

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                 88 LQLWMSNKRSLSPWGYSINHDPSRIPVDLPEARCLCLGCVNPFTWQEDRSMVSVPVF-SQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND ORGANISM IDENTIFICATION.
MEDLINE=97031826; PubMed=8877732;
Kennedy J., Rossi D.L., Zurawski S.M., Vega F. Jr., Kastelein R.A.,
Wagner J.L., Hannum C.H., Zlotnik A.;
"Mouse IL-11: a cytokine preferentially expressed by alpha beta TCR +
CD4-CD8-T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
-i- COUTION: WAS OFFICINALLY (REF.1) THOUGHT TO BE FROM MOUSE BUT, ON THE BASIS OF SUBSEQUENT WORK (REF.2 AND REF.3), HAS BEEN SHOWN TO BE OF RAT ORIGIN.
45 GQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEAD---- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Last Sequence update)
01-MRR-2002 (Rel. 41, Last annotation update)
Interleukin-17 precursor (IL-17) (Cytotoxic T lymphocyte-associated antiqen 8) (CTLA-8).
III7 OR CTLA8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rouvier E., Luciani M.F., Mattei M.-G., Denizot F., Golstein P.; "CTLA-8, cloned from an activated T cell, bearing AU-rich messenger RNA instability sequences, and homologous to a herpesvirus saimiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Interferon Cytokine Res. 16:611-617(1996).
                                                                            ----THQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL
                                   31 GOGRPGPLAPGP---HOVPLDLVSRMKPYARMEEYERNIEEMVAOLRNSSELAORKCEVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERLEDININ-17.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GECNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM IDENTIFICATION.
MEDLINE=9619901; PUDNEd=8654948;
YAO Z. Timour M., Painter S., Fanslow W., Springs M.K.;
"Complete nucleotide sequence of the mouse CTLA8 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytokine; Glycoprotein; T-cell; Antigen; Signal
                                                                                                                                                        156 LVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCV 192
                                                                                                                                                                                            147 VPVRRRLCPPP----PRTGPCRQRAVMETIAVGCTCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEMATOPOIETIC CYTOKINES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                 150 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93294300; PubMed=8390535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunol. 150:5445-5456(1993).
                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L13839; AAA37490.1;
                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 168:223-225(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
94
63
                                                                                                                                                                                                                                                                                             IL17_RAT
Q61453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene."
```

7

Page

```
Ouery Match
Best Local Sim
Matches 38;
                                                                                                                                                                                                                                             HNF6_HUMAN
 DISULFID
            CARBOHYD
                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha.
                                                                                                           92
 FT
                                                                                                           Qγ
                                                                                                                                 q
                                                                                                                                                          ò
                                                                                                                                                                                qq
                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                       2
                                                                                              42 LPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADT 101
                                                                                                                                             HQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRR 161
                                                                                                                                                            62 LNRSTSPWTLSRNEDPDRYPSVIWEAQCRQKCVNAE-GKLDHHMNSVLIQQEILVLKRE 120
                                                                       Gaps
                                                                                                                      21 IPQSSVCPNAEANNFLQNVKVNLKVINSL---SSKASSRRPS------DY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BALB/C; TISSUE-Thymocytes;
MEDLINE-97031826; PubMed-887732;
Kennedy J., Rossi D.L., Zurawski S.M., Vega F. Jr., Kastelein R.A.,
Wagner J.L., Hannum C.H., Zlotnik A.;
"Mouse IL-17: a cytokine preferentially expressed by alpha beta TCR
CD4-CD8-T cells ";
J. Interferon Cytokine Res. 16:611-617(1996).
                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Interleukin-17 precursor (IL-17) (Cytotoxic T lymphocyte-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: RESTRICTED TO A SUBSET OF ACTIVATED T-CELLS.
-i- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 168:223-225(1996)
-!- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND
HEMATOPOLETIC CYTOKINES (BY SIMILARITY)
-!- SUBUNIT: HOMODIMER (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                       33;
                                                Length 150;
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 I -> L (IN REF. 3).
16876 MW; EF13F33EDF9D689F CRC64;
                                                DB 1;
                                                                        55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine; Glycoprotein; T-cell; Antigen; Signal.
                                            / Match 13.8%; Score 148.5; DB :
Local Similarity 29.4%; Pred. No. 3.4e-07, Nes 45; Conservative 20; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERLEUKIN-17.
BY SIMILARITY.
                                                                                                                                                                                                                                                                               158 AA.
                                                                                                                                                                                                          P--CSRDGSGLPTPGAFAFHTEFIHVPVGCTCV 192
                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129/SV; TISSUE=T-cell; MEDLINE=96194901; PubMed=8654948;
                                                                                                                                                                                                                                                                          11.72_MOUSE STANDARD;
06.2386; 06.0971;
01.00V-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last seque)
01.MAR-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 12-158 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U43088; AAB05222.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA93253.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25
158
147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:107364; Ill7.
                                                                                                                                                                                                                                                                                                                                                    antigen 8) (CTLA-8).
IL17 OR CTLA8.
                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
          150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
          SEQUENCE
                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                 IL17_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                     Matches
                                                                                                                                                                                            162
FT
                                                                                              ò
                                                                                                                    g
                                                                                                                                                                 g
                                                                                                                                                                                            ò
                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                 ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-368 FROM N.A., AND VARIANT ALA-75.
MEDLINE=99420592; PubMed=10491763;
Meoller A.M., Ek J., Durviaux S.M., Urhammer S.A., Clausen J.O.,
Eiberg H., Hansen T., Rousseau G.G., Lemaigre F.P., Pedersen O.;
"Hepatccyte nuclear factor 6: associations between genetic variability and type II diabetes and between genetic variability and estimates of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Furuta H., Horikawa Y., Wang Y.-Q., Bell G.I.; "Isolation and characterization of the human hepatocyte nuclear factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS THE CONSENSUS SEQUENCE
5-5-DHWATTGAYTHWAD.3' ON A VARIETY OF GENE PROMOTERS SUCH AS THOSE
OF HHE3B AND TTR. IMPORTANT FOR LIVER GENES TRANSCRIPTION.
-1- SUBUNIT: BINDS DNA AS A MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UBCO; Q9UMR6; Q99744;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hepatccyte nuclear factor 6 (HNF-6) (One cut domain family member 1).
ONECUTI OR HNF6A OR HNF6.
                                                                                                                                                                                                                                                                                     RPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRL 151
                                                                                                                                                                                                                                                                                                                                          65 RPSDYL-----NRSTSPWTLHRNEDPDRYPSVIWEAOCRHORCVNAE-GKLDHHMNSVLI 118
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Samadani U., Costa R.H.;
Yeast one-hybid cloning of the partial human cDNA for hepatocyte
nuclear factor 6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                N-LINKED (GLCNAC. . .) (POTENTIAL).
3505C143435F4653 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Furuta H., Wang Y.-O., Bell G.I.; "The sequence of human mRNA for the hepatocyte nuclear factor-6
                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS 1 CUT DOMAIN.
-!- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                            DB 1; Length 158;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                               152 LOSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCV 192
                                                                                                                                                                                                       35;
                                                                                                                                                   Score 148.5; DB Pred. No. 3.6e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   465 AA.
                                                                                                                                                                                          ; Pred. No. 3.6e 13; Mismatches
   BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diabetologia 42:1011-1016(1999).
                                                              17490 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 174-465 FROM N.A.
                                                                                                                                                         13.8%;
37.6%;
                                                                                                                                                                                       Similarity 37.698; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insulin secretion."
                                                              158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
102
71
```

œ

Page

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
HNF6_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                              Matches
 pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                        11;
 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                               73 ASHRGRHERPSAT-----TQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY-- 120
                                                                                                                                                                                                                                                                                                                                                                                                                            269 -----REPNPSVTGAQVSNGSNSGQMEEINTKEVAQ-------RITTELKRYSI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 POKLAFAECLCR--GCID------ARTGRETAALNSVRL-----LQSLLVLR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-ocr-2001 (Rel. 40, Created)
16-ocr-2001 (Rel. 40, Last sequence update)
16-ocr-2001 (Rel. 40, Last annotation update)
16-ocr-2001 (Rel. 40, Last annotation update)
ONECUTION (Rel. 40, Last annotation update)
ONECUTION HNF6A ON HNF6.
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                          18 AHHDPSLRGHPHSHGTPHCYSAEELPLGQAPP----HLLARGAKWGQALPVALVSSLEA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 AHHPAMLGRHGEQHLTP--TSAGMVPINGLPPHHPHAHLNAQG--HGQLLGTA-----
                                                                                                                                    SMART; SM00389; HOX; 1.
PROSITE: PS00027; HOMEOBOX_1; FALSE_NEG.
PROSITE: PS50071; HOMEOBOX_2; 1.
Transcription regulation; Homeobox; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                        71;
                                                                                                                                                                                                                                                                                                                                     Length 465;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                      A -> T (IN REF. 3 AND 4).
S -> N (IN REF. 4).
Q -> H (IN REF. 4).
R -> K (IN REF. 4).
K -> Q (IN REF. 4).
W; F47F78957A6ECFC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                       53;
                                                                                                                                                                                                                                                                                                                                  8.0%; Score 85.5; DB 1; 25.8%; Pred. No. 1;
                                                                                                                                                                                                                                             /FTId=VAR_010729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               465 AA.
                                                                                                                                                                                                                                                                                                                                                       14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Liver;
Samadani U., Rausa F., Costa R.H.;
"Mouse hepatocyte nuclear factor-6 cDNA.";
          or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                           POLY-SER.
P -> A.
                                                                                                                                                                                                         POLY-HIS.
POLY-HIS.
                                                                                                                                                                                              HOMEOBOX.
                          EMBL; AF035581; AAD02033.1; --
EMBL; AF035580; AAD02033.1; --
EMBL; U96173; AAD00826.1; --
EMBL; Y17739; CAB50769.1; --
TRANSFAC; TA03286; --
TRANSFAC; T03286; --
MIM; 604164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                              InterPro; IPR003350; CUT.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                        51023 MW;
                                                                                                                 Pfam; PF02376; CUT; 1.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 25.8 Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                             Polymorphism
                                                                                                                                                                                     369
444
                                                                                                                                                                                                                                                                                                       165 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                        69
124
455
75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 RRPCSR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 LAACKR 372
                                                                                                                                                                           Activator; FDNA_BIND DNA_BIND DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HNF6_MOUSE
008755;
                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                 DOMAIN
DOMAIN
VARIANT
                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
HNF6_MOUSE
õ
                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is, in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                         -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS THE CONSENSUS SEQUENCE 5'-DHWATTCAYTWWD-3' ON A VARIETY OF GENE PROMOTERS SUCH AS THOSE OF HNF3B AND TTR. IMPORTANT FOR LIVER GENES TRANSCRIPTION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 ASHRGRHERPSAT-----TQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY-- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----REPNPSVTGAQVSNGSNSGQMEEINTKEVAQ------RITTELKRYSI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POKLAFAECLCR--GCID------ARTGRETAALNSVRL-----LQSLLVLR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HNF6_RAT STANDARD; PRT; 465 AA. p7512; 08875; 16.0CT-2001 (Rel. 40, Last sequence update) 16.0CT-2001 (Rel. 40, Last sequence update) 16.0CT-2001 (Rel. 40, Last annotation update) 16.0CT-2001 (Rel. 40, Last annotation update) 0.0CT-2001 (Rel. 40, Last annotation update) 10.0CT-2001 (Rel. 40, Last annotation update) 11.0CT-2001 (Rel. 40, Last 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 AHHDPSLRGHPHSHGTPHCYSAEELPLGQAPP----HLLARGAKWGQALPVALVSSLEA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEDBOX_1; FALSE_NEG.
PROSITE; PS50071; HOMEDBOX_2; 1.
Transcription regulation; Homeobox; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                -:- SUBUNIT: BINDS DNA AS A MONOMER (BY SIMILARITY).
-: SUBCELLULAR LOCATION: NUCLEAR.
-:- SIMILARITY: CONTAINS 1 CUT DOMAIN.
-:- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A770D27DD5AAC896 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ilarity 25.8%; Pred. No. 1;
Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.0%; Score 85.5; 25.8%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-HIS.
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUT.
HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50952 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U95945; AAB53863.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02376; CUT; 1.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
124
450
465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 RRPCSR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 LAACKR 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA_BIND
DNA_BIND
```

121 PQKLAFAECLCR--GCID------ARTGRETAALNSVRL-------LQSLLVLR

-----REPNPSVTGAQVSNGSNSGQMEEINTKEVAQ------RITTELKRYSI 310

269

óλ qq ò g δ

---TQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY--

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS THE CONSENSUS SEQUENCE 5'-DHWATTGAYTWWD-3' ON A VARIETY OF GENE PROMOTERS SUCH AS THOSE OF HNE'BA AND THE. IMPORTANT FOR LIVER GENES TRANSCRIPTION. THE AFFINITY OF HRF-GALPHA AND HNF-GBETA FOR DNA DIFFERS DEPENDING ON THE TARGET SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BRAIN, SPLEEN AND TESTIS.
-i- SIMILARITY: CONTAINS 1 CUT DOMAIN.
-i- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEOBOX PROTEINS.
                                                                                   "Hepatocyte nuclear factor 6, a transcription factor that contains a novel type of homeodomain and a single cut domain."; Proc. Natl. Acad. Sci. U.S.A. 93:9460-9464(1996).
                                                                                                                                                                                                                                                                                                                                   MEDLINE-97042457; PubMed-8887657; Samadani U., Costa R.H.; "The transcriptional activator hepatocyte nuclear factor 6 regulates
                                                                                                                                                                                                            Lannoy V.J., Buerglin T.R., Rousseau G.G., Lemaigre F.P.;
"Isoforms of hepatocyte nuclear factor-6 differ in DNA-binding properties, contain a bifunctional homeodomain, and define the new ONECUT class of homeodomain proteins.";
J. Biol. Chem. 273:13552-13562(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBGUNIT: BINDS DNA AS A MONOMER.
SUBGELLGLAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA;
ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> AESAMGGSVPSLRITSGGPQLSVPPLP (IN
                                                    Lemaigre F.P., Durviaux S.M., Truong O., Lannoy V.J., Hsuan J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcription regulation; Homeobox; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BD651267FD7AC896 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOFORM BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00027; HOMEOBOX_1; FALSE_NEG PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY - SER
             STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver; MEDLINE-96382488; PubMed-8790352;
                                                                                                                                                                                                                                                                                                                                                                                           liver gene expression.";
Mol. Cell. Biol. 16:6273-6284(1996)
SEQUENCE FROM N.A. (ISOFORM ALPHA)
                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM BETA).
                                                                                                                                                                                             MEDLINE=98256275; PubMed=9593691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Activator; Alternative splicing DNA_BIND 283 369 CU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001356; Homeobox.
Pfam; PF02376; CUT; 1.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X96553; CAA65389.1;
EMBL; Y14933; CAA75150.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003350; CUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138
460
368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00389; HOX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSFAC; T03257; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 AA;
                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T03258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  455
368
                                                                      Rousseau G.G.;
                                                                                                                                                                            STRAIN-WISTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                          novel
```

```
RAMEDINE-20190006; PubMed=10731132;

RA Adams M.D., Ceniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Holt P.W., Hoskins R.A., Galle R.F.,
RA Gacrge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Davi I., Dietz S.M.,
A horbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischman W.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Lasko P., Lei Y., Levitsky A.A., I.J., Wei M.-H., Ibegwan C.,
A Munt S.M., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Ralson D.R., Navon K., Nusskern D.R., Pacleb J.M.,
RA Ralson D.R., Navon K., Nusskern D.R., Scheelter F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sulb H., Wang Y.,
Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang Y.,
                                                                                                                                                                                                         Drosophila melanogaster.

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                        SEGUENCE FROM N.A. (LONG ISOFORM).
MEDILTNE-92154670; PubMed-1346755;
Tamkun J.W., Deuring R., Scott M.P., Kissinger M., Pattatucci A.M.,
Raufman T.C., Rennison J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Brahma: a regulator of Drosophila homeotic genes structurally related to the yeast transcriptional activator SNF2/SWI2."; Cell 68:561-572(1992).
                                            BRM_DROME STANDARD; PRT; 1638 AA. P25439, G9VUW5; O9VUM6; D16.0CT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Homeotic gene regulator (Brahma protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BERKELEY;
RESULT 15
BRM_DROME
```

11;

us-09-854-208-3.rsp

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
                                                                                                                         -1- FUNCTION: MAY ACT AS COACTIVATOR, ASSISTING ONE OR MORE DEDICATED
                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
-!- DEVELOPMENTAL STACE: HIGHEST EXPRESSION IN UNFERTILLIZED EGGS AND
                                                                                                                                       TRANSCRIPTIONAL ACTIVATORS OF ANT-C AND BX-C HOMEOTIC GENES. CAN COUNTERACT THE REPRESSIVE EFFECT OF POLYCOMB PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWART; SM00490; HELLUC; 1.

PROSITE: PS00633; BROMODOMAIN_1; 1.

PROSITE: PS50014; BROMODOMAIN_2; 1.

PEOSITE: PS50014; BROMODOMAIN_2; 1.

Bovelopmental protein; Transcription regulation; Nuclear protein;
Activator; Bromodomain; Hellcase; ATP-binding; Alternative splicing.

GLN/PRO-RICH.
                                                                                                                                                                                                                                           EARLY EMBRYOS.
-- MISCELIANEOUS: -- SIMILARIY: CONTAINS 1 BROMODOMAIN.
--- SIMILARIY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G -> A (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
D -> Y (IN REF. 1).
W). A4494B29F4F2E42A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASP/GLU-RICH (ACIDIC).
ARG/LYS-RICH (BASIC).
ASP/GLU-RICH (ACIDIC).
ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (POTENTIAL).
DEGH BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BROMODOMAIN.
POLY-ASP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AE003529; AAF49557.1; --
EMBL, AE003529; AAF49558.2; --
EMBL, A42091; A42091;
FlyBase, F8900000212; brm.
InterPro: IPR001487; Bromodomain.
InterPro: IPR001410; DEAD.
InterPro: IPR001430; SNF2_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185088 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00439; bromodomain; 1. Pfam; PF00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam. PF00176; SNF2_N: 1.
PRINTS: PR00503; BRCMODDMAIN.
SMART; SM00297; BROMO; 1.
SMART; SM00487; DEXDC: 1.
SMART; SM00499; HELICC: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M85049; AAA19661.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1410
1432
1513
1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1443 151
1631 163
121 12
122 22
687 68
1638 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                798
900
1385
1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
```

ä

Gaps

RHERPSATTQCPVLR-----PEEVLEADTH--QRSISPWRYRVDTDEDRYPQKLA 125

78

g &

δ

q

52 PGAYGHPMQHGPP----GQGPPGHHMPPHHQGMIFSKGPHMGMQMP----PIGPNMSPYQT 104

22 PSLRGHPHSHGTPHCYSAEELPLGQAPPH----LLARGAKWGQALPVALVSSLEAASHRG 77

7.9%; Score 84.5; DB 1; Length 1638; 22.2%; Pred. No. 5.2; Live 26; Mismatches 70; Indels 51

42; Conservative

Matches

Best Local Similarity

Query Match

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 23, 2002, 16:00:54 ; Search time 19.69 Seconds (without alignments) 961.381 Million cell updates/sec Run on:

Title: US-09-854-208-3
Perfect score: 1073
Sequence: 1 MTLLPGLLFLTWLHTCLAHH......FHTEFIHVPVGCTCVLPRSV 197

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 Total number of hits satisfying chosen parameters:

283138 segs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		rand protein initia beta-n-acetylhexos beta-N-acetylhexos 3-hydroxy-3-methyl pre-mRNA splicing hypothetical prote
SUMMARIES	B45351 146628 121334 121334 121334 150030 100030 100030 100030 100030 100030 100030 100030 100030 100030 100030 100030 100000	114100 F97670 AC2895 G84338 S64787 T00069
DB		2000000
% Query Match Length	151 150 150 150 150 150 150 150 150 150	466 639 639 405 503 1882
% Query Match	115.0 11.33.0 10.33.88.0 10.22.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7	7.22
Score	160.5 148.5 148.5 110 93.5 86.5 87.5 81.5 81.5 81.5 79 79 79 79 79 79 79 79 79 79	77 77 76.5 76.5
Result No.	23 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	222222 22222 2222 2222 2222 2222 2222 2222

probable oxidoredu	hypothetical prote	sensory box sensor	hypothetical prote	protein kinase (EC	hypothetical prote	CD27 antiqen precu	hypothetical 37.5K	transcription fact	probable transcrip	hypothetical prote	probable ddlA - My	iactA protein - Li	hypothetical prote	hypothetical prote	transcription fact
T35477	T00342	C75276	T50955	B49364	G72649	A46517	JH0657	S33724	I48694	T08262	B70673	T43164	T24914	B87571	A36389
~	7	~	~	N	~		N	~	~	7	~	7	~	7	7
296	1044	744	464	624	211	260	347	559	741	329	373	1080	181	362	466
7.1	7.0	7.0	6.9	6.9	6.9	6.9	6.9	6.8	6.8	8.9	8.9	9.8	8.9	9.9	6.8
92	75.5	75	74.5	74.5	74	74	74	73.5	73.5	73	73	73	72.5	72.5	72.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

 RESULT 1	
rnate names: hypotheti	saimiriine herpesvirus 1 (strain 11) cal protein ORF13
 A) Note: host Saimiri Sciureus (cor C, Date: 30-Sep-1993 #sequence_rev:	C.)Decens. saturation interportus 1 A;Note: host Saimiri sciureus (common squirrel monkey) C.)Date: 30.5ep-1993 #sequence_revision 30.5ep-1993 #text_change 16.Jul-1999
C,ACCESSION: B43331; J3880/ R;Nicholas, J.; Smith, E.P.; Coles Virology 179, 189-200, 1990	, L.; Honess, R.
A; Title: Gene expression in cells A; Reference number: A45351; MUID:	A;Title: Gene expression in cells infected with gammaherpesvirus saimiri: properties A;Reference number: A45351; MUID:91021021
 A; Accession: B45351 A; Molecule type: mRNA	
A; Cross-teferences: GB: M60286; NII	A. Nostance. 1 151 NAC. A.Cross references: GB:M60286; NID:g331040; PIDN:AAA46156.1; PID:g331042 B. Altrocht
submitted to the EMBL Data Library	', January 1992
A;Description: Primary structure of the herpesvirus saimiri genome A;Reference number: A36806	of the herpesvirus saimiri genome.
A; Accession: D36807	
A;Molecule type: DNA A;Residues: 1-151 <alb></alb>	
A;Cross-references: GB:X64346; NII	A;Cross-references: GB:X64346; NID:g60320; PIDN:CAA45636.1; PID:g60334
 K;AIDTECHT, J.C.; NICHOLAS, J.; B: J. Virol. 66, 5047-5058, 1992	.ler, D.; Cameron, K.K.; Blesinger, B.; Newman, C.;
 A; Title: Primary structure of the herpesvirus saimiri genome	herpesvirus saimiri genome.
 A; Contents: annotation: protein-coding frames	2333688 ding frames
A; Note: neither protein nor nucleotide sequence is given	otide sequence is given
C;Genetics:	
 A;Gene: 13 C;Superfamilv: saimiri herpesvirus immediate-earlv protein	immediate-early protein 2
 C; Keywords: early protein	
 Query Match 15.0%; Score 160.5; DB 1; Best Local Similarity 28.6%; Pred. No. 1.2e-07;	Score 160.5; DB 1; Length 151; Pred. No. 1.2e-07;
 Matches 46; Conservative 23	; Mismatches 57; Indels 35; Gaps 5;
QY 36 CYSAEELPLGQAPPHLLARGAKWC	36 CYSAEELPLGGAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
Db 18 CIVKSEITSAQTPRCLAAh	18 CIVKSEITSAQTPRCLAANNSFPRSVMVTLSIRNWNTSSKRAS 60
 Qy 96 VLEADTHQRSISPWRYRVDTDEDF	96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
 Db 61DYYNRSTSPWTLHRNEDQDF	:          :          :          :
 QY 156 LVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194	FHTEFIHVPVGCTCVLP 194
 Db 116 LVVRKGHQPCPNSFRLEKMLVTVGCTCVTP 145	:            FRLEKMLVTVGCTCVTP 145

```
Cipecies: Streptomyces sp.
Cibate: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 28-May-1999
Cibate: 170, 203-212, 1988
A.F. Title: Gene organization and structure of the Streptomyces lividans gal operon. A.F. Reference number: A28669, MUID:88086869
A.F. Residues: 1.395 ADA>
A.F. Residues: 1.395 ADA>
A.F. Residues: 1.395 ADA>
A.F. Coss-references: GB:M18953; NID:g153259; PIDN:AAA26748.1; PID:g153262
Cigenetics:
                                                                                                                                                                                                                   hypothetical protein F25D1.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Decies: Caenorhabditis elegans
C;Decies: Caenorhabditis elegans
C;Decies: Caenorhabditis elegans
C;Decies: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999
C;Accession: T21334
R;Kelly, P.
S;Reforence number: 219408
A;Reforence number: 219408
A;Reforence number: 219408
A;Reforence type: DAA
A;Reforence number: 219408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 ORSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 QC--PVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 RCDVPYADLDAALERLGDEEVRRLVRHVVTEDERVERVVALLESATPGASAPSWSRATP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTPHCYSAEELPLGQAPPHLLARG-AKW----GQALPVALVSSLEAASHRGRHERPSATT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 GTPSSSTPATSPSGRSPSTSPPRGCACWSSTPGSSTPTARASTASAARAARRAPRCWAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Gene: galK
C;Superfamily: galactokinase
C;Keywords: ATP; galactose metabolism; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.3%; Score 110; DB 2; 33.0%; Pred. No. 0.0054; iive 17; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.7%; Score 93.5; DB 29.5%; Pred. No. 0.53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 CSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPRS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 CDR-STGL---WNYVRSTELI--TVGCHSVLPRT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 29.58; Prea. no.
Matches 44; Conservative 15; Mismatches
| | | : | |||||||||---PFTFRVEKMLVGVGCTCV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           galactokinase (EC 2.7.1.6) - Streptomyces sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 ALNSVRLLQSLLVLRRRPCSRDGSGLPTP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: clone F25D1
C; Genetics:
A; Genetics:
A; Map position: 5
A; Map position: 5
A; Introns: 60/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                121 PEKC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytotoxic T-lymphocyte-associated antigen 8 precursor - mouse
N'Alternate names: immediate-early protein 2 (ORF13) homolog
S'Species: Mus musculus (house mouse)
C'Species: Mus musculus (house mouse)
C'Species: Musculu-1996 *sequence_revision 02-Jul-1996 *text_change 26-Aug-1999
C'Accession: I49623 *sequence_revision 02-Jul-1996 *text_change 26-Aug-1999
C'Accession: I49623 *Luciani, M.
J. Immunol. 150, 5445-5456, 1993
A;Title: CTLA-8, cloned from an activated T cell, bearing AU-rich messenger RNA instabil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A) Introns: 69/2
C; Superfamily: saimiri herpesvirus immediate-early protein 2
C; Superds: cytokine; glycoprotein; lymphocyte
F;1-14/Domain: signal sequence #status predicted <SIS>
F;15-14/Product: cytotoxic T-lymphocyte-associated antigen 8 #status predicted <MAT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
                                                                                                 cytotoxic T-lymphocyte-associated antigen 8 precursor - mouse
NAlternate names: CTAB protein
C;Species: Mus musculus (house mouse)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
C;Accession: JC46AB
C;Accession: JC46AB
C;Aritle: Complete nucleotide sequence of the mouse CTLAB gene.
A;Reference number: JC462B; MUID:96194901
A;Reference number: JC462B; MUID:96194901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Molecule type: DNA
A:Residues: 1-147 crao>
A:Cross-references: GB:U35108; NID:g1244499; PIDN:AAA93253.1; PID:g1244500
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 RPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 LNRSTSPWTLSRNEDPDRYPSVIWEAQCRHQRCVNAE-GKLDHHMNSVLIQQEILVLKRE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 LPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 HQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:L13839; NID:g293329; PIDN:AAA37490.1; PID:g293330 C;Genetics: A;Gene: Ctla-8 C;Superfamily: saimiri herpesvirus immediate-early protein 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 13.8%; Score 148.5; DB 2; Length 147; l Similarity 37.6%; Pred. No. 1.5e-06; 38; Conservative 13; Mismatches 35; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 IPOSSVCPNAEANNFLONVKVNLKVINSL---SSKASSRRPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 QQEILVLKREPES------CPFTFRVEKMLVGVGCTCV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 LQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.8%; Score 148.5; DB 2; 29.4%; Pred. No. 1.5e-06; iive 20; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: I49623
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-150 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 P--CSRDGSGLPTPGAFAFHTEFIHVPVGCTCV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 29.4%
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 38; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: ctla8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
```

4

12;

34;

Length 148; Indels s;

11; Gaps

Indels

79; DB 1;

Length 395;

11:11:49 2002

25

Sun Aug

```
transcription activator SNF2/SW12 homolog brm - fruit fly (Drosophila melanogaster) C; Species: Drosophila melanogaster c; Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Sep-1999 C; Accession: A42091 #squence_revision 18-Nov-1994 #text_change 20-Sep-1999 R; Tamkun, J.W.; Deuring, R.; Scott, M.P.; Kissinger, M.; Pattatucci, A.M.; Kaufman, T.A.; Tille: brahma: a regulator of Drosophila homeotic genes structurally related to the A; Reference number: A42091; MUID:92154670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Specias: Synechocystis sp.
C;Specias: Synechocystis sp.
C;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: 876371
R;Kanecko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                          88 CPVLRPEEVLEADTHQRS----ISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRET 143
                                                                                                                                                                78 RHERPSATTQCPVLR-----PEEVLEADTH--QRSISPWRYRVDTDEDRYPQKLA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 PCAYGHPMQHGPP----GQGPPGHHMPPHHQGMIFSKGPHMGMQMP---PTGPNMSPYQT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
      87
                                                                85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 PSLRGHPHSHGTPHCYSAEELPLGQAPPH----LLARGAKWGQALPVALVSSLEAASHRG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: Î-1638 <TAM>
A;Cross-references: GB:M85049; NID:g157011; PIDN:AAA19661.1; PID:g157012
A;Experimental source: iso-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: sequence extracted from NCBI backbone (NCBIN:82354, NCBIP:82360) C;Genetics:
   48 PPHLLARGAKWGQALPVAL-----VSSLEAASH-----RGRHERPSA----TTQ
                                                                28 PSRLILLG--WNRRAPLVLDQLRSTARTGSSVEVVADSAVPGPRGTEDRQPAGRDVRFRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: FlyBase:FBgn0000212
C;Superfamily: unassigned bromodomain proteins; bromodomain homology
C;Reywords: transcription regulation
F;1451-1506/Domain: bromodomain homology <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 FAECLCRGCIDARTGRETAALNSVRLLQS-----LLVLRRRPCSRD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.9%; Score 84.5; D
22.2%; Pred. No. 17;
tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S74322; MUID:97061201
A; Accession: S76371
                                                                                                                                                                                                                                                    144 AALNSVRLLQSLLVLRRRPCSRDGSG 169
                                                                                                                                                                                                                                                                                           Query Match 7.9%
Best Local Similarity 22.2%
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 GSGLPTPGA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 GPPIGPPGA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A42091
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: FlyBase:brm
                                                                                                                                                                                                                                                                                                              142
                                                                                                                                                                                                                                                                                                                                                                                                                                     A42091
                                                         Db
                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                       q
                                                                                                                             ò
                                                                                                                                                                                                                                                 Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical 31.7K protein (aphE region) - Streptomyces griseus
C;Species: Streptomyces griseus
C;Species: Jaceptomyces griseus
R;Heinzel, P.; Werbitzky, O.; Distler, J.; Piepersberg, W.
Archite: A second streptomycin resistance gene from Streptomyces griseus codes for strep
A;Feference number: Jaceptomycin resistance gene from Streptomyces griseus codes for strep
A;Reference number: Jaceptomycin resistance gene from Streptomyces griseus codes for strep
A;Reference number: Jaceptomycin resistance gene from Streptomyces griseus codes for strep
A;Residues: 1-297 <AHED
A;Residue
                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 RGSREVSPKIQVEWDLSKAKFDSGSEPRSGFYIAVVVDGBWGLLVGDSVKEAYARAKSAK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 PSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDAR--- 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 ---------TGRETAALNSVRLLQSLLV---LRRRPCSRDGSGLPTPGAFAF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 SVDSKQVLQIKRLRWKFRGNEKVEIDGVHVQISWDVYNWLFQSKSSGDGGGGGGHAVFMF 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 GLLFLTWLHTCLAHHDPSLRGHP---HSHGTPHCYSAEELPLGQAPP-HL----LA---- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGAK-----SSLEAASHRGRHER 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.0%; Score 86; DB 2; Length 297; Best Local Similarity 27.4%; Pred. No. 1.9; Matches 40; Conservative 15; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.1%; Score 86.5; DB 2; 23.0%; Pred. No. 2.3; tive 25; Mismatches 83;
303 A---ARRLPHLLP-RAGPGRRHGPGLRGP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 23.0%
les 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 HTE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           엽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
```

```
16;
                                                                                       A Status: preliminary
A Molecule type: DNA
A Residues: 1-553 <STO>
A Cross-references: GB:AE004444; GE
A Experimental source: strain PAOI
C Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 IFPKELIQWGDQVKQAYDA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | : | | | 158 DIGEVNFQSGIIEVPQVC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --GAFAFHTEFIHVPVGC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                       A; Gene: PA0049
                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
                                                                                                                                                                                                                                                                                                                                                                                                                 26
                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    083640
hypothetical protein PA0049 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species Seudomonas aeruginosa
C;Species Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: D88640
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
                                                      NID:g1001484; PIDN:BAA10223.1; PID:g100159
to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 155/2; 189/3; 234/3; 268/3
C;Superfamily: transcription factor Pit-1; homeobox homology; POU domain homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
                                                                                                                                                                                      8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL:275711; PIDN:CAB00031.1; GSPDB:GN00019; CESP:K02B12.1
A; Experimental source: clone K02B12
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Feb-2000
C;Accession: T23218
                                                                                                                                                                                                                                                                                                                      267 HLSPIYGGFIDSKGPRYCPSIEDKIVRFADKESHQIFIEPEGRDIPELYIQGFSTGLPEN 326
                                                                                                                                                                                                                                                                                                LPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYP 121
                                                                                                                                                                                                                                                                                                                                                                          122 QKLA--FAECLCRGCIDARTGRETAA-----LNSVRLLQ--SLLVLRRRPCSRDGSGL 170
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 FLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVALVS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 FODWPHTPMLYQQPQLHFMLPQHDWAYPHLAQSLP----PPHHLTPS-----TAAVA 59
                                                                                                                                                                                                                       HHDPSLRGHPHSHGTPHCYSAEEL-------PLGQAPPHLLARGAKWG--QA
                                                                                                                                                                                  57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 SLEAASHRGRHERPSATTQCPVLR-PEEVLEADTHQRSISPW--RYRVDTDE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54; Indels
                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein K02B12.1 - Caenorhabditis elegans
                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Harris, B. Submitted to the EMBL Data Library, July 1996
A.Reference number: 219710
A.Accession: T23218
A.Status: preliminary: translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-325 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                             ; Score 82.5; DI
; Pred. No. 9.2;
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 81.5; Di
Pred. No. 5.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Mismatches
           A Molecule Lype: DNA
A; Residues: 1-635 <KAN>
A; Cross-references: EMBL:D64000; GB:AB001339;
A; Note: the nucleotide sequence was submitted
C; Superfamily: gidA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.6%;
                                                                                                                                               ch 7.7%;
1 Similarity 24.2%;
44; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 25.9%
les 29; Conservative
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: CESP:K02B12.1
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 PT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GT 419
                                                                                                                                             Query Match
Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                       19
                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
```

```
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82956; MUID:20437337
A;Accession: p83640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Status: preliminary
A.Molecule type: protein
A.Residues: 1-210 

C.Superfamily: 4-alpha-glucanotransferase / amylo-1,6-glucosidase

C.Superfamily: 4-alpha-glucanotransferase; hexosyltransferase; hydrolase; polysacc

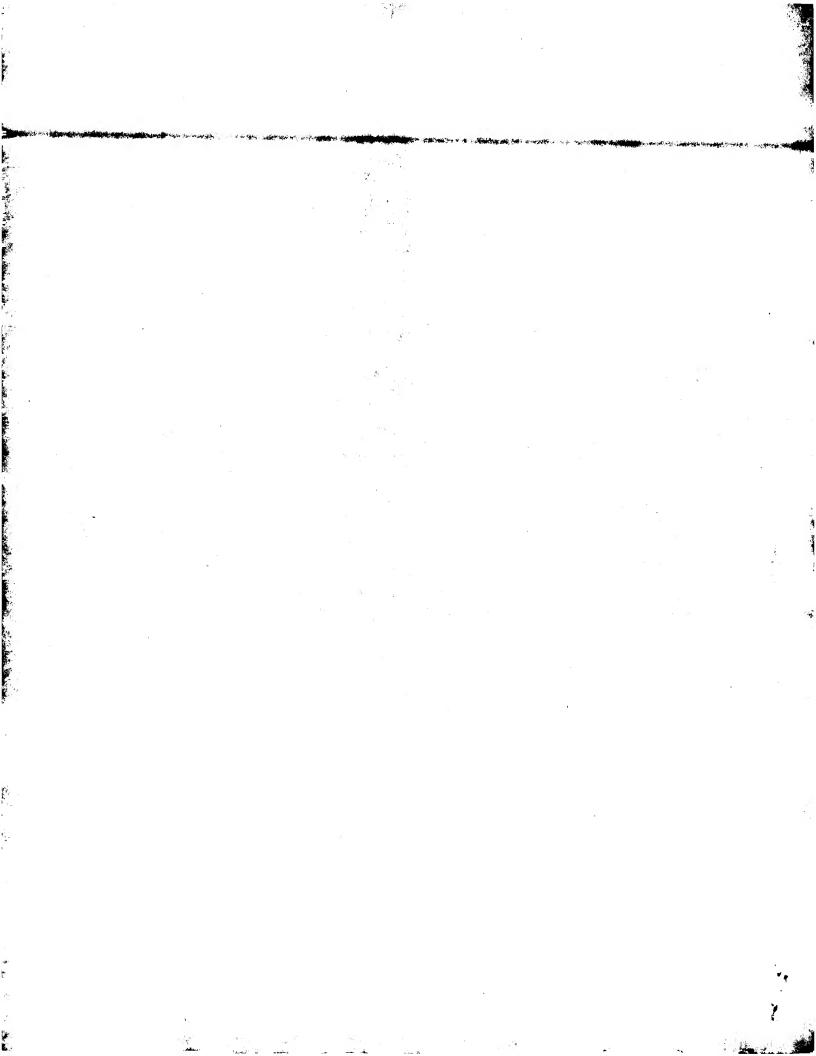
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: B40203
R;Yang, B.Z.; Ding, J.H.; Enghild, J.J.; Bao, Y.; Chen, Y.T.
J. Biol. Chem. 267, 9294-9299, 1992
A;Tille: Molecular cloning and nucleotide sequence of cDNA encoding human muscle glyc A;Reference number: A40203; MUID:92250533
                                                                                                                                                                                                                                                                   GB:AE004091; NID:g9945863; PIDN:AAG03439.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amylo-1,6-glucosidase (EC 3.2.1.33)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4-alpha-glucanotransferase (EC 2.4.1.25) / amylo-1,6-glucosidase (EC 3.2.1.. C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 ADTHORSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSV--RLLQSLL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 WLEAWNGRFHGSSAG---NDGIVYCPADSALPNYVLPLGSVTNPGTAPISLRGSGCNINP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LPSSTIV--SMACCASGSTKWNPAASPS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----AKWGQALPVALVSS-----LEAASHRGRHERPSATTQCPVLRPEEVLE 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 PSLRGHPHSHGT--PHCYS-AEELPLG---QAPPHLLARGAKWGQALPVALVSSLEAASH 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::| | | | : | | | : | | 362 PRRWLGYDSASRWRQNLPAQFSKASLPVRQLLAADTWRGIERPPGATSQA----AEGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 RGRHERPSAT------TQCPVLRPEEV---LEADTHQRSISPWRYRVDTDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----LGQAPPHLLARG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 RWLHEHPECAYNLVNSPHHKALWHLSCDVAEGRGVPALIENDHHMNSI-----RLIIWED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 RYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.5%; Score 80.5; DB 2; Length 210; 25.3%; Pred. No. 4.2; tive 17; Mismatches 76; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 VL--RRRPCSRDGSG---LPTPGAF-----AFHTEF----IHVPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 WLHTCLAHHDPSLRGHPHSHGTPHCYSAEELP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.5%; Score 81; 24.2%; Pred. No.
```

```
C;Accession: 137386
R;Tian, Q;; Taupin, J; Elledge, S.; Robertson, M.; Anderson, P.
Exp. Med. 182, 865-874, 1995
A;Title: Fas-activated serine/threonine kinase (FAST) phosphorylates TIA-1 during Fas A;Reference number: 137386; MUID:95378805
A;Accession: 137386
A;Acteus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-549 <RES>
A;Cross-references: EMBL:X86779; NID:g1006658; PIDN:CAA60448.1; PID:g1006659
                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 LVVQETQLSSKVVQKLVLPFGRLNY------LPLEQQFMPCLER--ILAREA-GVAPL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LVSSL-EA-----ASHRGRHERPSATTQCPVLRPEEVLEADTH- 102
96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGC-IDARTGRETAALNSVRLLQ 153
                              ------QRSISPW---RYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 LHTCLAHHDPSLRGHPHSHGTPHCYSAEE--LPLGQAPPHLLARGAKWGQALPVA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.4%; Score 79; DB 2; Length 549; 28.6%; Pred. No. 17; Live 12; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: fast
C;Superfamily: human fas-activated serine/threonine kinase
                                                                                                                                                                                    fas-activated serine/threonine kinase - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                completed: August 23, 2002, 16:02:16 ne: 82 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.4%
Best Local Similarity 28.6%
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 NSVRLLQSLLVLRRRP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 ATVNILMSLCQLRCLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search comp
Job time: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103
  δλ
                                                 pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                óλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      рp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                          C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C; Accession: A70509
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajanfream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Reference number: A70500; MUID:98295987
A; Reference number: A70500; MUID:98295987
A; Rocession: A70509
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-411 <COL>
A; Cross-references: GB:298260; GB:AL123456; NID:93261826; PIDN:CAB10927.1; PID:e129939;
C; Genetics: Rv1230C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        overexpr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ling integr B-look contedration protein, GOA - numan Cispectes: Homo sapiens (man)
Cispectes: Homo sapiens (man)
Cispectes: Homo sapiens (man)
Cibate: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 14-Dec-2001
Cibate: 14-Dec-2001
Cibate: 14-Dec-2001
Cibate: 14-Dec-2001
Cibate: 14-Dec-2001
Cibate: 14-Dec-2001
Cibate: Da.A.; Meije, C.B.; van Dartel, M.; Leenstra, S.; IJlst-Keizers, H.; Das Biochem. Biophys. Res. Commun. 286, 574-579, 2001
A; Reference number: JC7753; MUID: 21402356; PMID: 11511098
A; Recession: JC7753
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecules: 1-638 cVAN>
A; Cicomment: This protein, a member of the subfamily of the ring finger proteins, has an as well.
Cicomment: This protein, a member of the subfamily of the ring finger proteins, has an as well.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 PPTSFRVAVATISAPPPPMIVNSPGALGIPAMALSAYRNAELKMAAAAP---GCGVSWNL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 LAGIGRIESMHA---NGGATDARGTAIQPIYGPTLDGTLPGNEIIIQSSVGNRVTYARAM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 GPMQFLPGTWARYATDGDDDGVADPQNLFDSTLAAARYLCSGGLNLRDPAQVMAALLRYN 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRP------EEVLEAD-----THQRSI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGLLFLTWLHTCLAHHDPSLRGHPHSHGTP----HCYSAEELPLGQAPPHLLARGAKWGQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 EELPLGQAPPHLLARGAKWGQALPVAL -- VSSLEA -- ASHRGRHERPSATTQCPVLRPEE 95
                                                 hypothetical protein Rv1230c - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SP-----W-RYRVDTDED-----RYPQKLAFAECLCRGCIDARTGRET-AAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 80; DB 2; Length 411; Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.5%; Scor.
23.7%; Pred. No. 9.c.
...e. 23; Mismatches "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ring finger B-box coiled-coil protein, GOA - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.4%; Score 79.5; D
30.3%; Pred. No. 18;
:ive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 23.79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||: |::|
|| NSMPYAQNVL 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 NSVRLLQSLL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 17q24-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Si
Matches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

12;

Gaps 65

70;



12, Appl 112, Appl 1, Appli 1, Appli 6, Appli 9, Appli 8, Appli 19, Appli 19, Appli

Sequence 1 Sequence 2 Sequence 6 Sequence

ALIGNMENTS

Sequence 1 Sequence 4 Sequence 2 Sequence 1 Sequence 7 Sequence 2 Sequence 9 Sequence 9 Sequence 9 Sequence 9 Sequence 1 Sequence 1

Appl Appli Appli

```
US-08-318-947A-16
US-08-795-303-16
US-08-795-303-4
US-08-261-822A-12
PCT-US95-07744A-12
US-08-477451-7
US-08-918-206-1
US-08-422-699A-9
US-08-422-699A-9
US-08-449-645A-19
US-08-06-195-06-19
US-08-06-195-06-19
US-08-06-1019-2
US-09-600-776-6
US-09-600-776-6
US-09-600-776-6
US-09-600-776-6
US-09-600-776-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 153 amino acids
amino acid
    CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics J
STREET: 87 Cambridge
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-514-014-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cambridge
Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02140
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                              \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-514-014-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
    STATE:
    (without alignments)
367.597 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Appl
Sequence 12, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                            1 MTLLPGLLFLTWLHTCLAHH......FHTEFIHVPVGCTCVLPRSV 197
                                                                                                                                                 Search time 13.09 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence Sequence 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sedinence Sedine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.5
Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -08-432-994A-4
-08-432-994A-8
-08-620-694A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-034-810-6
US-09-022-255-8
US-09-022-255-8
US-09-022-253-8
US-09-022-250-8
US-09-022-259-8
US-09-022-259-8
US-08-432-994A-4
US-08-432-994A-8
US-08-432-994A-8
US-08-422-620-694A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -09-022-260-7
                                                                                                                                                                                                                                                                                                                                                                                     231628 segs, 24425594 residues
                        version -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                 August 23, 2002, 16:00:49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                           protein search, using sw model
                                                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
                      GenCore (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
                                                                                                                                                                                                                               US-09-854-208-3
1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                          Copyright
                                                                                                                                                                                                                                                                                                                        BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table: .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160.5
160.5
160.5
160.5
160.5
160.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
150.5
                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                         OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maximum
                                                                                                                                                 Run on:
```

```
e,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 LEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 153;
Sequence 12. Application US/08514014

Patent No. 5707829

GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: Kelleher, Kerry
APPLICANT: Carlin, McKeough
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
TITLE OF INVENTION: BLOODED THEREBY
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/514,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.1%; Score 173; DB 1; 39.0%; Pred. No. 9.4e-13; iive 16; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: =: -
- = =
                                                                                                                                                                                                                                                                 3: Genetics Institute, Inc.
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G1600
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 39.09
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

Sequence Sequence

09-034-810-4

Sequence

Sequence

3-08-432-994A-2 3-08-432-994A-10 3-08-432-994A-6

Sequence

 $^{\circ}$ 

g δ

```
Mi.Sha
Mi.Sha
Neben, Steven
Giannotti, JoAnn
Golden'Fleet, Margaret
Golden'Fleet, Margaret
Golden'Fleet, Margaret
                                                                                                                                                                                                                 APPLICANT: Neben, Steven
APPLICANT: Giannotti, Joann
APPLICANT: Giannotti, Joann
APPLICANT: Golden'Fleet, Margaret
APPLICANT: Golden'Fleet, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 LEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PALENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/034,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 VLRRR--PCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 VVRRKHQGCS------VSFQLEKVLVTVGCTCVTP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.1%; Score 173; DB 3; 39.0%; Pred. No. 1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 39.0%; Pred. No. 1.1
Best Local Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,239
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08685239 Patent No. 6074849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kelleher, Kerry
Carlin, McKeough
Goldman, Samuel
Pittman, Debra
                                                      Carlin, McKeough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                           Goldman, Samuel
Pittman, Debra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 876-5851 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 163 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 87 Cambridger
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-09-034-810-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Giannott
APPLICANT: Golden'F
TITLE OF INVENTION:
                                                                                                                                                                                 Mi, Sha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                        APPLICANT:
                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-685-239-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
60 MSRNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRNLGCINAQ-GKEDISMNSVPIQQETL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 LEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Kerry
APPLICANT: Kelleher, Kerry
APPLICANT: Carlin, McKeough
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
STREET: 87 cambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.1%; Score 173; DB 2; Length 153; 39.0%; Pred. No. 9.4e-13; tive 16; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,823
FILING DATE: 10-APR-1997
CLASSIFICATION: 530
                                                                                      157 VLRRR--PCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                    |:||: || :||: || 119 vvrrkhqgcs-----vsfqlekvlvtvgcgctcytp 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 VLRRR--PCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/514,014
FILING DATE: 11-ANG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G16000
TELEPHONE: (617) 498-8224
TELEPHONE: (617) 498-8224
TELEPAX: (617) 476-8821
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08833823 Patent No. 5969093 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09034810
Patent No. 6043344
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 153 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 39.08
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-833-823-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02140
                                                                                                                                                                                                                                                                                                        RESULT 2
US-08-833-823-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-09-034-810-2
```

ä;

g

g

```
156 LVLRR--RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 LVVRKGHQPCPN-----SFRLEKMLVTVGCTCVTP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 2.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.0%; Score 160.5; 28.6%; Pred. No. 2.8
APPLICALLO.
FILING DATE: 7 AUGUST 12..
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTONREY/ABOTT INFORMATION:
NAME: PERKINS, PALTICIA Anne
REGISTRATION NUMBER: 34,695
FREEREMENCAPOCKET NUMBER: 2617-B
TRELECOMMUNICATION INFORMATION:
TRELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Herpesvirus Saimiri
ORF13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09034810 Patent No. 6043344
                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 151 amino acids TYPE: amino acid STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: Kelleher, Kerry
APPLICANT: Carlin, McKeough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear .
MOLECULE TYPE: protein HYPOTHETICAL: NO ANITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-620-694A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-034-810-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 LEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
16.1%; Score 173; DB 3; Length 16
Best Local Similarity 39.0%; Pred. No. 1e-12;
Matches 39; Conservative 16; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 VVRRKHQGCS------VSFQLEKVLVTVGCTCVTP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 VLRRR--PCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                      ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/620,694A FILLING DATE: 21 MARCH 1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/685,239
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15262
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08620694A Patent No. 5869286 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 amino acids
                                                                               CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
  NUMBER OF SEQUENCES: 9
                   CORRESPONDENCE ADDRESS:
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                          RY: USA
02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-620-694A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-685-239-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
```

```
APPLICANT: Kelleher, Kerry
APPLICANT: Carlin, McKeough
APPLICANT: Carlin, McKeough
APPLICANT: Dittman, Debra
APPLICANT: Mi, Sha
APPLICANT: Mi, Sha
APPLICANT: Giannotti, Joann
APPLICANT: Golden/Fleet, Margaret
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
                                                                                                                                                                   96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                                                                                                                                                                                                36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
Length 151;
                                                                                                               57; Indels
```

5,

```
96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No. 6072037el Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 CIVKSEITSAQTPRCLAA----NNSFPRSVMVTLSIRNWNTSSKRAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Apple, Version 6.0.1 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/09/022,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 LVLRR--RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.0%; Score 160.5; DB 3 28.6%; Pred. No. 2.8e-11; tive 23; Mismatches 57
       USSN 08/410,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
                ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PARTICIAL
NAME: PERKINS, PATTICIA Anne
REGISTRATION NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEPHONE: (206)587-0430
TELEPHONE: (206)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acids
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                          : Herpesvirus Saimiri
ORF13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09022696
Patent No. 6072037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: NO. 60720:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.0%
Best Local Similarity 28.6%
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; STRAIN:
US-09-022-255-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-022-696-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ----DYYNRSTSPWTLHRNEDQDRYPSVIWEAKCRYLGCVNA-DGNVDYHMNSVPIQQEI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/0902255;
Patent No. 6072033;
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporation
STREET: 51 university Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 15.0%; Score 160.5; DB 3; Length 1 Best Local Similarity 28.6%; Pred. No. 2.8e-11; Matches 46; Conservative 23; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 CIVKSEITSAQTPRCLAA-----NNSFPRSVMVTLSIRNWNTSSKRAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MACCOSOFT Word for Apple, Version 6.0.1
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 LVVRKGHQPCPN-----SFRLEKMLVIVGCTCVTP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 LVLRR--RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/034,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Brown, Soctt A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/685,239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 151 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-09-034-810-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-022-255-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

35;

Indels

s)

```
61 ----DYYNRSTSPWTLHRNEDQDRYPSVIWEAKCRYLGCVNA-DGNVDYHMNSVPIQQEI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                            36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
                                                                                                                                                                                                                                                                                                                                                        Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCE: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 CIVKSEITSAQTPRCLAA----NNSFPRSVWVILSIRNWNTSSKRAS----
                                                                                                                                                                                                                                                                                                                                                     Query Match 15.0%; Score 160.5; DB 3; Length Best Local Similarity 28.6%; Pred. No. 2.8e-11; Matches 46; Conservative 23; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 LVLRR--RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JMBER: USSN 08/538,765
7 AUGUST 1995
                         NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15262
TELECOMMUNICATION INFORMATION:
TELEPAN: (617) 498-8224
TELEPAN: (617) 497-5821
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
FILING DATE: 01-MARCH-1996
APPLICATION NUMBER: USSN 08/538,71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 2617-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09022253 Patent No. 6096305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 06
FILING DATE: 23 MARCH 1995
      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                 LENGTH: 151 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-685-239-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 7
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98101
                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-09-022-253-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Giannotti, Joann
APPLICANT: Giannotti, Joann
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 CIVKSEITSAQIPRCLAA----NNSFPRSVMVTLSIRNWNTSSKRAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 LVLRR--RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.0%; Score 160.5; DB 3 28.6%; Pred. No. 2.8e-11; tive 23; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                      ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELEPHONE: (206)587-0430
TELEPHONE: (206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/685,239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: Herpesvirus Saimiri
STRAIN: ORF13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08685239 Patent No. 6074849
                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
  23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jacobs, Kenneth
APPLICANT: Kelleher, Kerry
APPLICANT: Carlin, McKeough
APPLICANT: Goldman, Samuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goldman, Samuel
Pittman, Debra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mi, Sha
Neben, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.03
Best Local Similarity 28.63
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
FILING DATE: 2 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          us-09-022-696-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-685-239-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
```

5

```
96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 CIVKSEITSAQTPRCLAA----NNSFPRSVMVTLSIRNWNTSSKRAS------
                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-022-259-8
Sequence 8, Application US/09022259
Sequence 8, Application US/09022259
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOSTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/022,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 LVLRR--RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.0%; Score 160.5; DB 3; Best Local Similarity 28.6%; Pred. No. 2.8e-11; Matches 46; Conservative 23; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USSN 08/410,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2617-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                             TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                  ANTI-SERSE: NO
ORIGINAL SOURCE:
ORGANISM: Herpesvirus Saimiri
STRAIN: ORF13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 0E
FILLING DATE: 23 MARCH 1995
CLASSIFICATION:
                      (206)587-0430
(206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 51 Uni
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: WA
COUNTRY: US
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                       ; STRAIN:
US-09-022-260-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ----DYYNRSTSPWTLHRNEDQDRYPSVIWEAKCRYLGCVNA-DGNVDYHMNSVPIQQEI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
                                                                                                                                                                                                                                                                                                                                                                                            Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
APPLICANT: Ensilow, William
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 CIVKSEITSAOTPRCLAA----NNSFPRSVMVTLSIRNWNTSSKRAS-----
                                                                                                                                                                                                                                                                                                                                                                                     ;; Score 160.5; DB 3; Length 1;
Fred. No. 2.8e-11;
23; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 OPERATING SYSTEM: Apple Operating System 7.5.5 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/022,260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 LVLRR--RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                 No. 6096305 Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                              ORGANISM: Herpesvirus Saimiri
STRAIN: ORF13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09022260 Patent No. 6100235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
RECISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
                          TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 28.6%;
Matches 46; Conservative 23
                      (206)587-0430
                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: prot
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                    ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                       ; STRAIN:
US-09-022-253-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-022-260-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
```

., 2

```
96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ----DYYNRSTSPWTLHRNEDQDRYPSVIWEAKCRYLGCVNA-DGNVDYHMNSVPIQQEI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
                                                                                                                                                                                                                                                                                                                                                                                            15.0%; Score 160.5; DB 4; Length 151; 28.6%; Pred. No. 2.8e-11; Live 23; Mismatches 57; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Golstein, Pierre
APPLICANT: Rouvier, Eric
APPLICANT: Rouvier, Francois
APPLICANT: Lebecque, Serge J. E.
APPLICANT: Djossou, odile
APPLICANT: Banchereau, Jacques
TITLE OF INVENTION: PUBLFIED MAMMALIAN CTLA-8 ANTIGENS AND
TITLE OF INVENTION: RELATED REAGENTS
CORRESPONDENCE: 10
CORRESPONDENCE: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 LVLRR--RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 LVVRKGHOPCPN-----SFRLEKMLVTVGCTCVTP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: DNAX Research Institute 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/432,994A FILING DATE: 02-MAY-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/250,846
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/177,747
FILING DATE: 05-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08432994A Patent No. 6274711
                             TELERAX: (206)
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                  ORGANISM: Herpesvirus Saimiri
STRAIN: ORF13
    TELECOMMUNICATION INFORMATION:
                        (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 28.69
Matches 46; Conservative
                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                          ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-08-432-994A-4
                                                                                                                                                                                                                                                                                                         ; STRAIN:
US-09-022-257-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ----DYYNRSTSPWTLHRNEDQDRYPSVIWEAKCRYLGCVNA-DGNVDYHMNSVPIQQEI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 CIVKSEITSAQTPRCLAA-----60
                                                                                                                                                                                                                                                                                                                                                                                              Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-02-257-8

Sequence 8, Application US/0902257

Patent No. 6197525

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Foralow, Malaine

TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17

NUMBER OF SEQUENCE: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Apple Fower Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 LVLRR--RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.0%; Score 160.5; DB 4; 28.6%; Pred. No. 2.8e-11; tive 23; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USSN 08/410,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PAITIGIA Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
ORGANISM: Herpesvirus Saimiri
STRAIN: ORF13
                               INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 06
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                          Query Match. 15.0%
Best Local Similarity 28.6%
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                          ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: WA
COUNTRY: USZ
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                           US-09-022-259-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                  ς,
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ---- DYYNRSTSPWTLHRNEDQDRYPSVIWEAKCRYLGCVNA-DGNVDYHMNSVPIQQEI 115
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08432994A

Patent No. 6274711

GENERAL INFORMATION:
APPLICANT: Golstein, Pierre
APPLICANT: Rouvier, Eric
APPLICANT: Fossiez, Francois
APPLICANT: Lossiez, Francois
APPLICANT: Diossou, Odile
APPLICANT: Banchereau, Jacques
TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-8 ANTIGENS AND
TITLE OF INVENTION: RELATED REAGENTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                                                                                                                                                                                57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 CIVKSEITSAQTPRCLAA----NNSFPRSVMVTLSIRNWNTSSKRAS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 LVLRR--RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

FILING DATE: US/08/432,994A FILING DATE: 02-MAY-1995
                                                                                                                                                                                                                                                                                                                                                     Score 160.5; DB 4
Pred. No. 2.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/250,846
FILING DATE: 27-MX-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/177,747
FILING DATE: 05-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,203
FILING DATE: 14-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: DNAX Research Institute
901 California Avenue
                                          NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: DX0388K3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                  TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 anino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                       15.0%;
FILING DATE: 14-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 28.69
                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-432-994A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-432-994A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
3,
                                                                                                                                                                                                                                                                                                                                                                                                                       99 ADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                  Length 155;
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                  Query Match 14.7%; Score 158; DB 4; Best Local Similarity 39.8%; Pred. No. 5.7e-11; Matches 39; Conservative 11; Mismatches 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 RREPPHCPN-----SFRLEKILVSVGCTCVTP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 RRRP -- CSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: August 23, 2002, 16:01:11 Job time: 22 sec
                                                             DX0388K3
                 NAME: Ching, Edwin P.
REGISTATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX038
TELECOMMUNICATION INFORMATION:
TELEFONE: 415-85-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 8:
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
                                                                                                                                                                                       : 155 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-432-994A-8
                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                            TYPE: amin
TOPOLOGY:
                                                                                                                                                                                         LENGTH:
```